

09914191 082401  
533 Rec'd PCT/PTO 24 AUG 2001

FORM PTO-390 (REV. 11-2000)		U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE	ATTORNEY'S DOCKET NUMBER 1377-0170P
TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371			U.S. APPLICATION NO. (If known, see 37 CFR 1.5) <b>09914191</b>
INTERNATIONAL APPLICATION NO. PCT/IE00/00026	INTERNATIONAL FILING DATE February 28, 2000	PRIORITY DATE CLAIMED February 26, 1999	
TITLE OF INVENTION IDENTIFICATION OF GENES HAVING A ROLE IN THE PRESENTATION OF DIABETIC NEPHROPATHY			
APPLICANT(S) FOR DO/EO/US BRADY, Hugh R.; GODSON, Catherine M.; MARTIN, Finian M.; McMAHON, Ruth A.; MURPHY, Madeline A.			
Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:			
<p>1. <input checked="" type="checkbox"/> This is a <b>FIRST</b> submission of items concerning a filing under 35 U.S.C. 371.</p> <p>2. <input type="checkbox"/> This is a <b>SECOND</b> or <b>SUBSEQUENT</b> submission of items concerning a filing under 35 U.S.C. 371.</p> <p>3. <input checked="" type="checkbox"/> This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39 (1).</p> <p>4. <input checked="" type="checkbox"/> The US has been elected by the expiration of 19 months from the priority date (Article 31).</p> <p>5. <input checked="" type="checkbox"/> A copy of the International Application as filed (35 U.S.C. 371(c)(2))</p> <p>a. <input checked="" type="checkbox"/> is transmitted herewith (required only if not transmitted by the International Bureau). WO 00/50637</p> <p>b. <input checked="" type="checkbox"/> has been transmitted by the International Bureau.</p> <p>c. <input type="checkbox"/> is not required, as the application was filed in the United States Receiving Office (RO/US).</p> <p>6. <input type="checkbox"/> An English language translation of the International Application as filed (35 U.S.C. 371(c)(2)).</p> <p>a. <input type="checkbox"/> is transmitted herewith.</p> <p>b. <input type="checkbox"/> has been previously submitted under 35 U.S.C. 154(d)(4)</p> <p>7. <input checked="" type="checkbox"/> Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3)).</p> <p>a. <input type="checkbox"/> are transmitted herewith (required only if not transmitted by the International Bureau).</p> <p>b. <input type="checkbox"/> have been transmitted by the International Bureau.</p> <p>c. <input type="checkbox"/> have not been made; however, the time limit for making such amendments has NOT expired.</p> <p>d. <input checked="" type="checkbox"/> have not been made and will not be made.</p> <p>8. <input type="checkbox"/> An English language translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).</p> <p>9. <input checked="" type="checkbox"/> An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).</p> <p>10. <input type="checkbox"/> An English language translation of the annexes of the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).</p>			
Items 11. to 20. below concern document(s) or information included:			
<p>11. <input checked="" type="checkbox"/> An Information Disclosure Statement under 37 CFR 1.97 and 1.98-International Search Report (PCT/ISA/210)</p> <p>12. <input type="checkbox"/> An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.</p> <p>13. <input checked="" type="checkbox"/> A FIRST preliminary amendment.</p> <p>14. <input type="checkbox"/> A SECOND or SUBSEQUENT preliminary amendment.</p> <p>15. <input type="checkbox"/> A substitute specification.</p> <p>16. <input type="checkbox"/> A change of power of attorney and/or address letter.</p> <p>17. <input type="checkbox"/> A computer-readable form of the sequence listing in accordance with PCT Rule 13ter.2 and 35 U.S.C. 1.821-1.825.</p> <p>18. <input type="checkbox"/> A second copy of the published international application under 35 U.S.C. 154(d)(4).</p> <p>19. <input type="checkbox"/> A second copy of the English language translation of the international application under 35 U.S.C. 154(d)(4).</p> <p>20. <input checked="" type="checkbox"/> Other items or information:</p> <p>1.) PCT Substitute Claims Letter w/ International Preliminary Examination Report (PCT/IPEA/409) and claims</p> <p>2.) Eleven (11) sheets of Sequence Listing</p> <p>3.) Twenty-four (24) sheets of Formal Drawings</p>			

JC05 Rec'd PCT/PTO 24 AUG 2007

U.S. APPLICATION NO. <b>097514191</b>	INTERNATIONAL APPLICATION NO PCT/IE00/00026	ATTORNEY'S DOCKET NUMBER 1377-0170P
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21. ☒ The following fees are submitted:

BASIC NATIONAL FEE (37 CFR 1.492(a)(1)-(5): Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO. ....	\$1,000.00	CALCULATIONS	PTO USE ONLY																
International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO .....	\$860.00																		
International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.445(a)(2)) paid to USPTO. ....	\$710.00																		
International preliminary examination fee (37 CFR 1.482) paid to USPTO but all claims did not satisfy provisions of PCT Article 33(1)-(4) .....	\$690.00																		
International preliminary examination fee (37 CFR 1.482) paid to USPTO and all claims satisfied provisions of PCT Article 33(1)-(4). ....	\$100.00																		
<b>ENTER APPROPRIATE BASIC FEE AMOUNT =</b>																			
Surcharge of \$130.00 for furnishing the oath or declaration later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(e)).		\$ 860.00																	
<table border="1" style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th style="width: 20%;">CLAIMS</th> <th style="width: 20%;">NUMBER FILED</th> <th style="width: 20%;">NUMBER EXTRA</th> <th style="width: 20%;">RATE</th> </tr> </thead> <tbody> <tr> <td>Total Claims</td> <td>11 - 20 =</td> <td>0</td> <td>X \$18.00</td> </tr> <tr> <td>Independent Claims</td> <td>1 - 3 =</td> <td>0</td> <td>X \$80.00</td> </tr> <tr> <td>MULTIPLE DEPENDENT CLAIM(S) (if applicable)</td> <td colspan="2">None</td> <td>+ \$270.00</td> </tr> </tbody> </table>		CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE	Total Claims	11 - 20 =	0	X \$18.00	Independent Claims	1 - 3 =	0	X \$80.00	MULTIPLE DEPENDENT CLAIM(S) (if applicable)	None		+ \$270.00	\$ 0	
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE																
Total Claims	11 - 20 =	0	X \$18.00																
Independent Claims	1 - 3 =	0	X \$80.00																
MULTIPLE DEPENDENT CLAIM(S) (if applicable)	None		+ \$270.00																
<b>TOTAL OF ABOVE CALCULATIONS =</b>		\$ 860.00																	
<input checked="" type="checkbox"/> Applicant claims small entity status. See 37 CFR 1.27. The fees indicated above are reduced by 1/2.		\$ -430.00																	
<b>SUBTOTAL =</b>		\$ 430.00																	
Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(f)).		\$ 0																	
<b>TOTAL NATIONAL FEE =</b>		\$ 430.00																	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property +		\$ 0																	
<b>TOTAL FEES ENCLOSED =</b>		\$ 430.00																	
		Amount to be: <b>refunded</b>	\$																
		<b>charged</b>	\$																

a. ☒ A check in the amount of \$ **430.00** to cover the above fees is enclosed.

b. ☐ Please charge my Deposit Account. No. \_\_\_\_\_ in the amount of \$ \_\_\_\_\_ to cover the above fees.  
A duplicate copy of this sheet is enclosed.

c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 02-2448.

**NOTE:** Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

Send all correspondence to:  
**Birch, Stewart, Kolasch & Birch, LLP** or Customer No. 2292  
**P.O. Box 747**  
**Falls Church, VA 22040-0747**  
**(703)205-8000**

Date: August 24, 2001

By Gerald M. Murphy, Jr. #36,623  
Gerald M. Murphy, Jr., #28,977



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09/914191 4  
Rec'd PCT/PTO 19 DEC 2001  
BOX SEQUENCE  
PATENT  
1377-0170P

IN THE U.S. PATENT AND TRADEMARK OFFICE

Applicant: BRADY et al. Conf.: 9468  
Appl. No.: 09/914,191 Group: UNASSIGNED  
Filed: August 24, 2001 Examiner: UNASSIGNED  
For: IDENTIFICATION OF GENES HAVING A ROLE IN  
THE PRESENTATION OF DIABETIC NEPHROPATHY

AMENDMENT

Assistant Commissioner for Patents  
Washington, DC 20231

December 19, 2001

Sir:

In response to the Notice to File Missing Requirements mailed October 19, 2001, the following amendments and remarks are respectfully submitted in connection with the above-identified application.

In the Specification:

Please delete the Sequence Listing of record. Please insert the Substitute Sequence Listing enclosed herewith immediately after the claims.

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REMARKS

Enclosed herewith in full compliance to 37 C.F.R. §§1.821-1.825 is a Substitute Sequence Listing to be inserted into the specification as indicated above. The Substitute Sequence Listing in no way introduces new matter into the specification. Also submitted herewith in full compliance to 37 C.F.R. §§1.821-1.825 is a disk copy of the Substitute Sequence Listing. The disk copy of the Sequence Listing, file "1377-0170P.ST25.txt", is identical to the paper copy, except that it lacks formatting.

If necessary, the Commissioner is hereby authorized in this, concurrent, and future replies, to charge payment or credit any overpayment to Deposit Account No. 02-2448 for any additional fees required under 37 C.F.R. § 1.16 or under 37 C.F.R. § 1.17; particularly, extension of time fees.

Respectfully submitted,

BIRCH, STEWART, KOLASCH &amp; BIRCH, LLP

By *Gerald M. Murphy, Jr.* *Do 46,061*  
Gerald M. Murphy, Jr., #28,977

GMM/MAA/BCF  
1377-0170P

P.O. Box 747  
Falls Church, VA 22040-0747  
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Attachments:      Disk Copy of Sequence Listing  
                     Paper Copy of Sequence Listing  
                     Copy of Notice to Comply

(Rev. 03/27/01)

09/914191  
JC05 Rec'd PCT/PTO 24 AUG 2001

PATENT  
1377-0170P

IN THE U.S. PATENT AND TRADEMARK OFFICE

Applicant: BRADY, Hugh Redmond et al.  
Int'l. Appl. No.: PCT/IE00/00026  
Appl. No.: New Group:  
Filed: August 24, 2001 Examiner:  
For: IDENTIFICATION OF GENES HAVING A ROLE IN THE  
PRESENTATION OF DIABETIC NEPHROPATHY

PRELIMINARY AMENDMENT

**BOX PATENT APPLICATION**

Assistant Commissioner for Patents  
Washington, DC 20231

August 24, 2001

Sir:

The following Preliminary Amendments and Remarks are respectfully submitted in connection with the above-identified application.

AMENDMENTS

IN THE SPECIFICATION:

Please amend the specification as follows:

Before line 1, insert --This application is the national phase under 35 U.S.C. § 371 of PCT International Application No. PCT/IE00/00026 which has an International filing date of February 28, 2000, which designated the United States of America and was published in English.--

Docket No. 1377-0170P

**IN THE CLAIMS:**

Please amend the claims as follows:

3. (Amended) A method according to Claim 1, wherein the concentration of glucose is greater than 5mM.

4. (Amended) A method according to Claim 1, wherein the mesangial cells are subjected to mechanical strain.

5. (Amended) A method according to Claim 1, wherein transforming growth factor  $\beta 1$  (TGF- $\beta 1$ ) is added to the culture medium.

6. (Amended) A method according to Claim 1, wherein the possibility of differential expression due to hyperosmolarity is excluded.

7. (Amended) A method according to Claim 1, wherein the gene so differentially expressed is a gene which includes a sequence selected from:

- 1) SEQ ID NOS: 1-3;
- 2) SEQ IS NO: 4;
- 3) SEQ ID NO: 5; and
- 4) SEQ ID NO: 6.

8. (Amended) Use of a gene identified by a method according

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to Claim 1, as a diagnostic marker for the progression and presentation of diabetic nephropathy.

9. (Amended) Use of a gene identified by a method according to Claim 1, as an index of disease activity and the rate of progression of diabetic nephropathy.

10. (Amended) Use of a gene identified by a method according to Claim 1, as a basis for identifying drugs for use in the prevention and/or therapy of diabetic nephropathy.





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**VERSION WITH MARKINGS SHOWING CHANGES MADE**

The specification has been amended to provide cross-referencing to the International Application.

The claims have been amended as follows:

3. (Amended) A method according to Claim 1 [or 2], wherein the concentration of glucose is greater than 5mM.

4. (Amended) A method according to [any preceding claim]Claim 1, wherein the mesangial cells are subjected to mechanical strain.

5. (Amended) A method according to [any preceding claim]Claim 1, wherein transforming growth factor  $\beta 1$  (TGF- $\beta 1$ ) is added to the culture medium.

6. (Amended) A method according to [any one of Claims 1-5]Claim 1, wherein the possibility of differential expression due to hyperosmolarity is excluded.

7. (Amended) A method according to [any one of Claims 1-6]Claim 1, wherein the gene so differentially expressed is a gene which includes a sequence selected from:

- 1) SEQ ID NOS: 1-3;
- 2) SEQ IS NO: 4;

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3) SEQ ID NO: 5; and

4) SEQ ID NO: 6.

8. (Amended) Use of a gene identified by a method according to [any one of Claims 1-7]Claim 1, as a diagnostic marker for the progression and presentation of diabetic nephropathy.

9. (Amended) Use of a gene identified by a method according to [any one of Claims 1-7]Claim 1, as an index of disease activity and the rate of progression of diabetic nephropathy.

10. (Amended) Use of a gene identified by a method according to [any one of Claims 1-7]Claim 1, as a basis for identifying drugs for use in the prevention and/or therapy of diabetic nephropathy.

24/PRTS

09/914191  
JC05 Rec'd PCT/PTO 24 AUG 2001  
PCT/IE00/00026DescriptionIdentification of genes having a role in the presentation of diabetic nephropathy.

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Technical Field

This invention relates to the characterisation and identification of genes which play a role in diabetes, more particularly in the onset and progression of diabetic nephropathy and to the use of genes so characterised and/or identified as diagnostic markers for diabetic nephropathy and as the basis of drug development programmes.

10

Background Art

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Between 2-5% of the population develops diabetes mellitus and 20-30% of diabetics develop diabetic nephropathy. The latter accounts for over 30 % of end-stage renal failure (E.S.R.F.) requiring dialysis or transplantation in western society. The pathological hallmark of diabetic nephropathy is glomerulosclerosis due to accumulation of extracellular matrix proteins in the glomerular mesangium. Mesangial matrix accumulation reflects both increased synthesis and decreased degradation of extracellular matrix (ECM) components, and correlates with the clinical onset of proteinuria, hypertension and progressive kidney failure. Hyperglycaemia is a major stimulus for mesangial cell matrix production in diabetic nephropathy. The mechanisms by which hyperglycaemia perturb mesangial cell function are still being

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appreciated and include direct effects of high extracellular glucose levels and indirect effects transduced through alterations in glomerular haemodynamics and through the actions of advanced glycosylation end products.

5

Propagation of mesangial cells under conditions of high ambient glucose has proved a useful *in vitro* model with which to probe the molecular basis for mesangial matrix accumulation in diabetes, attributable to hyperglycaemia. Specifically, exposure of cultured mesangial cells to high glucose stimulates *de novo* synthesis of ECM components, such as type IV collagen, fibronectin and laminin, and other products that are accumulated *in vivo* (Ayo, S.H., *et al.* (1990) *Am.J. Pathol.* 136, 1339-1348; Wahab, N.A., *et al.* (1996) *Biochem. J.* 316, 985-992; and Ayo, S.H., *et al.* (1991) *Am. J. Physiol.* 260, F185-15 F191).

In view of the high morbidity and mortality rate from diabetic nephropathy in diabetics there is a need to identify stimuli which affect the onset and progression of diabetic nephropathy with the aim of preventing such onset or inhibiting or limiting the progression thereof.

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### Disclosure of Invention

The invention provides a method for identifying a gene having a role in the presentation of diabetic nephropathy, which method comprises culturing mesangial cells in a medium in the presence of a concentration of glucose sufficient to induce differential expression of a

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gene susceptible to such differential expression and identifying the gene so induced by suppression subtractive hybridisation.

5 Preferably, the mesangial cells are cultured in the presence of a concentration of glucose sufficient to induce up-regulation of a gene susceptible to such up-regulation.

10 Further, preferably, the concentration of glucose is greater than 5 mM.

A concentration of 5 mM falls within the normal range of plasma glucose levels in a healthy human subject (4.2 – 6.4 mmol/l).

15 The concentration of glucose used is suitably in the range 5-30 mM. The concentration of 30 mM was chosen as the classic "*in vitro*" model of diabetic nephropathy which induces changes in mesangial function that mimic human disease. This level is also encountered in many diabetics *in vivo*.

20 In one embodiment, the mesangial cells are subjected to mechanical strain.

25 In a further embodiment, transforming growth factor  $\beta 1$  (TGF- $\beta 1$ ) is added to the culture medium.

Suppression subtractive hybridisation (SSH) is a method based on suppressive PCR that allows creation of subtracted cDNA libraries for the identification of genes differentially expressed in response to an experimental stimulus (Gurskaya, N.G., *et al.* (1996) *Anal. Biochem.* 240, 90-97). SSH differs from earlier subtractive methods by including a normalisation step that equalises for relative abundance of cDNAs within a target population. This modification should enhance the probability of identifying increased expression of low abundance transcripts, and represents a potential advantage over other methods for identifying differentially regulated genes such as differential display-PCR (DD-PCR) (Liang, P., and Pardee, A.B. (1992) *Science* 257, 967-97) and cDNA-representation difference analysis (Hubank, M., and Schatz, D.G., (1994) *Nucleic Acid Res.* 22, 5640-5648).

To date we have used SSH to identify 150 genes differentially induced when human mesangial cells were exposed to high extracellular glucose (defined herein as 30 mM versus 5 mM) *in vitro*. These genes included:

(a) known regulators of mesangial cell activation in diabetic nephropathy, namely fibronectin, caldesmon, thrombospondin and plasminogen activator inhibitor-1;

(b) novel genes; and

(c) genes whose induction by high glucose has not previously been reported as hereinafter described.

Prominent among the latter were genes encoding cytoskeleton-associated proteins and connective tissue growth factor (CTGF), a  
5 modulator of fibroblast matrix production. We have also demonstrated elevated CTGF mRNA levels in glomeruli of rats with streptozotocin-induced diabetic nephropathy.

10 In one aspect of the invention, the possibility of differential expression due to hyperosmolarity is excluded.

Hyperosmolarity is, however, a component of diabetic nephropathy and thus hyperosmolarity may represent a mechanism  
15 through which high glucose induces differential expression of certain genes having a role in the presentation of the disease.

For example, we have shown that mannitol provoked less mesangial cell CTGF expression *in vitro* than high glucose, excluding  
20 hyperosmolarity as the key stimulus.

High glucose also stimulated expression of transforming growth factor  $\beta 1$  (TGF- $\beta 1$ ) and addition of TGF- $\beta 1$  to mesangial cells triggered CTGF expression. Anti-TGF- $\beta 1$  antibody blunted CTGF expression  
25 induced by high glucose. Together, these data suggest that (1) high glucose stimulates mesangial CTGF expression by TGF $\beta 1$ -dependent

and independent pathways, and (2) CTGF may be a mediator of TGF- $\beta$ 1-driven matrix production within a diabetic milieu.

CTGF may therefore be an attractive target for design of novel  
5 anti-sclerotic therapies for diabetic glomerulosclerosis.

CTGF derived from mesangial cells is a potential stimulus for increased synthesis of ECM proteins and mesangial expansion in diabetic nephropathy. The mechanisms by which high glucose triggers  
10 mesangial cell CTGF and, indeed, TGF- $\beta$ , mRNA expression remain to be defined. Possible upstream triggers of CTGF transcription in response to high glucose include *de novo* synthesis of diacylglycerol (DAG) and subsequent activation of protein kinase C (PKC) (DeRubertis, F.R., and Craven, P., (1994) *Diabetes* 43, 1-8 and Fumo P.,  
15 *et al.* (1994) *Am. J. Physiol.* 267, F632-F638), non-enzymatic glycation end-products (Brownlee, M., *et al.* (1984) *Ann. Intern. Med* 101, 527-537 and Cohen, M.P., and Ziyadeh, F.N. (1994) *Kidney Int.* 45, 475-484) increased activity of the polyol pathway and disordered myoinositol metabolism (Goldfarb, S., *et al.* (1991) *Diabetes* 40, 465-  
20 471 1991) or through the recruitment of locally generated growth factors such as TGF- $\beta$ 1 and other mediators. (Sharma K., and Ziyadeh, F.N., (1995) *Diabetes* 44, 1139-1146).

TGF- $\beta$ 1 has been implicated as the key mediator of extracellular  
25 matrix accumulation in diabetic nephropathy and other chronic renal disease. Several studies have reported increased expression of TGF- $\beta$ 1 in renal glomeruli in human and experimental models of diabetes (Park,



I., *et al.* (1997) *Diabetes* 46, 473-480; Sharma, K., (1996) *Diabetes* 45, 522-530). Short term administration of TGF- $\beta$ 1 neutralising antibodies attenuates overexpression of mRNAs encoding matrix components and glomerulosclerosis in the STZ mouse model of diabetes (Park, I., *et al.* (1997) *Diabetes* 46, 473-480). CTGF shares some of the biological actions of TGF- $\beta$ 1 such as stimulation of cell proliferation and extracellular matrix protein synthesis in fibroblasts. When considered in this context, the results described herein suggest that TGF- $\beta$ 1 may promote mesangial matrix production, in part, by inducing CTGF synthesis. TGF- $\beta$ 1 has a complex profile of biological activities that includes pro-inflammatory, pro-fibrotic and anti-inflammatory effects. By targeting CTGF it may be possible to attenuate the sclerosis-inducing effects of TGF- $\beta$ 1 while preserving its more desirable anti-inflammatory activities.

Novel genes identified by the method according to the invention are identified herein as IHG (*I*ncreased in *H*igh *G*lucose) and DHG (*D*own in *H*igh *G*lucose) and are represented by genes which include the following sequences 1, 3 and 4:

1) TTGGAATAGTTCTTGCTTTATAAAAATAGTACTGCGATTAAA  
AAAAAAGCACTTCTGCCAAAGGAACCATGTTCCAACACCGCA  
AACAAGGTGTTCTGCTTAAACAGAGTAAGATACACCACCCCC  
ATCCATCCCTTCCTTCCCTGTTCCCCTCCCAACTTGAGTTGTGT  
CATTCGCACCAAGTGTCTTGGGTGGTAGGGATGCTACAGCCAC  
CTAAGGCAAGGAGCCCTGGGAGGTGGGAGGGCTTGCATGGTT  
AAGCACACCAGAACTGAAGCGCAAAAGGGTCAGCTGTCTTCA

TCTAGAATCTCTGGATGTTTCCTTCCAGAAAGCATCCCCGATGA  
TATCGCAGTGCAAGGGGCACTGGCTTTGTCCTGGTCCGGGTCAC  
TGCCATCTTTTTTTCCTTCCATTTCTGTTGGCAGCTTAATTTCTTT  
TGTCATCACTTCATCCACCTTCTGCCATATCAACACAGTCCCTT  
5 TCCTATACATCGGCAGCTCATTATTATAGTTGATGTTGAATTC  
AGAAAACAAAATCTCATTCTTGTCTGCTGNAAGAGTTCCTGT  
AATCTCCCTTGGGCTTGTACTGGTGTAGTCCAGATTGTTG  
(SEQ ID NO: 1)  
.....  
10 .....GGTCCTTTAA  
AGTCTGGTTGCTGGGATACACCACGACTCTTCCGGTCAAAGCC  
TGGGGGATACAGAAGGGGCTRGTCCTCAAAGTAATCCCGCCA  
ATAAAACAYATAGCTGGAGGCAAACCTGGGAGGYCACGTGAGT  
CATGAACTTTACTGGCTCTTCTTTTAAACCAATTGGTTTTCCGC  
15 TTGWACACAAAGCTGTACTCATCACTCTGTCCATAACGCGAT  
CACAATATCCTCTAGTTCTTCCATCACAGTCTGCGCACATTG  
GTCATCAGCTGGAGAGCACGGCTGTCATTGGGTTTTGCAAAGT  
TGTGCTTCTCAGCAAACCGATGGAAATTCCGGCCGTCCAGCCG  
NACTACCACCCAGCAGTGTGCCAGGCAGGTGTCGTCAGCCTC  
20 GAAGTCCCTCACGTACTCGAACTTGCTTTTTTGCCATGGTCGCC  
CCCAATCTCAGGTACCGTCTCAGAGTGATGGAAATGGTGGCC  
AAGGAATCGTGAACCTTAACCTTTACAGGCGCCCCACATTCTAC  
ACGCGGAAAGGAAAGGGCCAGATAGCCCCGCCCCGGAAGTG  
TTCTCTTCGTGGCTACTCTAGCCGTAGGGCGGTCATAGTCTCT  
25 CTCGSCTCTCCCTGKAGTTCTTAAMCYCCAGGGAAARAGGA  
TGGAGGTTTAGGTTCCCTCCGTTAGCACCTTCCACGCTTGCTTCT  
TCCTCCTCCCGGTCTGCGGCAAATCAGTCTCACGAGGTTTTTA

AAAATTATTTTTATCTGCTGGCCTT (SEQ ID NO: 2)  
.....ATGACACAAATATTAG  
GATTTTATTTTTACTATTATCCACCAGCAACAAGATATCAAAC  
ACTGGTTCTGTGATTATTTAATGGTGAAAAAGTTGAATAAATC  
5 AATTTAGTATACCCATATGTTGGAATATTGAGTCCATTTTTCTT  
TTAAAAATCACACTTTGGAATAATTGATGATACTGGCAAATGC  
TCAAGCTGAGTGGAAAAATATATAAACATTGTATAGGCGAAT  
AATTCCAATCTTGTGCATTCCCTGTGTAAACCTACATACACAA  
AAAGAAAAAAGACTGAAAGGAACCATCCACAATGCTTTGATC  
10 GGGAAAGACGGAGAAACAAAGTGTTAATTTTCTTAAGTATAG  
TTTTNGGTGTATTCCAGATTTTCTACAAGTTAATA (IHG-1) (SEQ  
ID NO: 3);

2)GTACTTTGGATTTGGTTAACCTGTTTTCTTCAAGCCTGAGGT  
15 TTTATATACAAACTCCCTGAATACTCTTTTTGCCTTGTATCTTC  
TCAGCCTCCTAGCCAAGTCCTATGTAATATGGAAAACAAACA  
CTGCAGACTTGAGATTCAGTTGCCGATCAAGGCTCTGGCATTTC  
AGAGAACCCTTGCAACTCGAGAAGCTGTTTTTATTTTCGTTTTT  
GTTTTGATCCAGTGCTCTCCCATCTAACAACCTAAACAGGAGCC  
20 ATTTCAAGGCGGGAGATATTTTAAACACCCAAAATGGTTGGG  
TCTGATTTTCAAACTTTTAAACTTCACTACTGATGATTCTGCA  
CGCTAAGGCGAATTTGGTCCAAACACATAAGTGTGTGTGTTTT  
GTATACACTGTATGACCCCAACCCCAAATCTTTGTATTGTCCAC  
ATTCTCC IHG-2 (SEQ ID NO: 4);

25

3)AGAAGCAATTTAGGAANCCNACAGNAAANAAATGCTGTTTT  
ATAGGAGAGAAAACACGGCACACCAAGGTAAAGTAGTTTGTA

GACGATGTTGAATAGGTTTCAGGTACAGGTCAATGCAGTGATG  
AGGAAAGCACCTANGTATACTTGACAGATAGTCCCCTTTGCTT  
AACACCCAACTCCTCCACCCTGTGCAGTTTNNCTTGTGCCAGT  
GATCACAGGATTCGCTGAGTGAATTACCATAATTGGATTTAAT  
5 TCACGAAGGGGATGTTTTTC (IHG-3) (SEQ ID NO: 5); and

4)ATTGATAGAGGCCCTGTTTCATGACATTTTCATGAGTTTCAAT  
ATGTTGTTTCAGCATGTTGTGAGGTGACTCTCAGCCCCTTTCCC  
ACTGAGATGGACTGTGGTGATGCTGTGAGGGTGTGACTGACA  
10 CACCTTCATGTGCCCAAGCATGGGTTTGATCACAGGTCACATG  
CAGTTTTTGGCATAGTAAATGTATCATTGTTCTTTTCCTCCCTC  
CTAAAGGAAACAGAGGAATCCACCTGTATGAGAGTGCCATGT  
AGGGATAAACTTAAAGGACAGATGACACATTGGTCATGTTTCG  
TGATAAGGAAA (DHG-1) (SEQ ID NO: 6).

15

The invention also provides SEQ ID NOS: 1-3, 5 and 6 set out above.

In initial studies the gene IHG-2 was assumed to be new.  
20 However, as hereinafter demonstrated IHG-2 was identified as being a  
formerly unknown part of the gremlin gene. We have found that  
mesangial cell gremlin mRNA levels are induced by high glucose,  
cyclic mechanical strain and TGF- $\beta$ 1 *in vitro*, and gremlin mRNA levels  
are elevated in the renal cortex of rats with streptozotocin-induced  
25 diabetic nephropathy *in vivo*. Gremlin expression was observed in  
parallel with induction of bone morphogenetic protein-2 (BMP-2), a  
target for gremlin in models of cell differentiation.

Gremlin, together with DAN and cerberus, are members of the cysteine knot super-family of proteins that have recently been shown to play important roles in limb development and neural crest cell differentiation (Hsu, D.R., *et al.* (1998) *Mol. Cell.* 1, 673-83; Zuniga, A., *et al.* (1999) *Nature* 401, 598-602). Of potential interest in the context of diabetic nephropathy, gremlin is a putative inhibitor of BMP-2 in models of neural crest cell differentiation. BMP-2 has recently been reported to have antiproliferative effects on mesangial cells.

The following Examples show that (a) IHG-2 is part of gremlin, (b) gremlin is expressed in diabetic nephropathy *in vivo*, (c) both glycemic and mechanical strain stimulate mesangial cell gremlin expression *in vitro*, (d) high glucose induces gremlin, in part, through TGF $\beta$ -mediated pathways, and (e) gremlin is a potential endogenous antagonist of BMPs within a diabetic glomerular milieu.

The invention also provides use of a gene identified by the method according to the invention:

1) as a diagnostic marker for the progression and presentation of diabetic nephropathy;

2) as an index of disease activity and the rate of progression of diabetic nephropathy; and

It is possible to generate mouse knock-out (k/o) models for genes identified in accordance with the invention and to generate

Fig. 6 is a 2 % agarose gel showing ethidium-stained PCR products as described in Example 3;

Fig. 7 is an autoradiograph of CTGF levels in the presence of TGF- $\beta$ 1 and TGF- $\beta$ 1 neutralising antibodies analysed by Northern Blot as described in Example 4;

5

Fig. 8 is a graph of the relative amount of CTGF mRNA as estimated by Phosphor Imager quantification as described in Example 4;

Fig. 9 is an autoradiograph of CTGF levels in the presence of varying amounts of glucose and TGF- $\beta$ 1 neutralising antibodies analysed by Northern Blot as described in Example 4;

10

Fig. 10 is a graph of the relative amount of CTGF mRNA as estimated by Phosphor Imager quantification as described in Example 4;

15

Fig. 11 is an autoradiograph of CTGF levels in the presence of varying amounts of glucose and PKC inhibitor GF102903X analysed by Northern Blot as described in Example 4;

20

Fig. 12 is a graph of the relative amount of CTGF mRNA as estimated by Phosphor Imager quantification as described in Example 4;.

Fig. 13 is a graphical representation of a BLAST output from the EST database as described in Example 6;

25



Fig. 14 is a graphical representation of the alignment of human gremlin and rat drn when compared using the BLAST algorithm as described in Example 6;

5 Fig. 15 is the sequence of mesangial cell gremlin cDNA;

Fig. 16 is an autoradiograph of IHG-2, gremlin, fibronectin and GAPDH mRNA levels analysed by Northern Blot as described in Example 7;

10

Fig. 17 is a graph of relative mRNA levels as estimated by Phosphor Imager quantification as described in Example 7;

15 Fig. 18 is an autoradiograph of gremlin, fibronectin and GAPDH mRNA analysed by Northern Blot as described in Example 7;

Fig. 19 is a further graph of relative mRNA levels as estimated by Phosphor Imager quantification as described in Example 7;

20 Fig. 20 is an autoradiograph of gremlin mRNA levels in the kidney cortex of a STZ-diabetic rat and an age matched control analysed by Northern Blot as described in Example 7;

25 Fig. 21 is a further graph of relative mRNA levels as estimated by Phosphor Imager quantification as described in Example 7;

Fig. 22 is an autoradiograph of gremlin, fibronectin and GAPDH mRNA levels analysed by Northern Blot as described in Example 8;

5 Fig. 23 is a graph of relative mRNA levels as estimated by Phosphor Imager quantification; and

Fig. 24 is a graphical representation of representative reactions of four independent experiments as described in Example 9.

10 The invention will be further illustrated by the following Examples:

#### Modes for Carrying Out the Invention

##### 15 Example 1

#### Identification of mesangial cell genes differentially induced by high glucose.

##### 20 a) Cell culture and streptozotocin-induced diabetic rats

Primary human mesangial cells were cultured as previously reported (Brady, H.R., *et al.* (1992) *Kidney Int.* 42, 480-487 and Denton, M.D., *et al.* (1991) *Am. J. Physiol.* 261, F1071-F1079). Cells (passage 25 7-11) were maintained in medium (Clonetics) containing either 5 mM or 30 mM D-glucose for 7 days. Culture medium was replenished three times during this period to maintain glucose levels in the desired range. To control for the effects of hyperosmolarity, mesangial cells were

cultured in media containing 5 mM glucose supplemented with 25 mM mannitol.

Male Munich-Wistar rats (260-290 g, Simonsen Laboratories) were rendered diabetic by treatment with streptozotocin (STZ; Sigma), 50 g/kg, intravenously as described previously (Zatz, R., *et al.* (1985). *Proc. Natl. Acad. Sci. USA.* 82, 5963-5967). At months 2 and 4 after induction of diabetic nephropathy (DN), rats were anaesthetized with intraperitoneal injection of pentobarbital (50 mg/kg), and the right kidney was excised and weighed immediately. Glomeruli were isolated from renal cortex by the standard sieving method (Brady, H.R. *et al.* (1992) and Denton, M.D. *et al.* (1991) *supra*). Glomerular isolation was completed within 20 minutes of removing the kidney. RNA extraction proceeded immediately thereafter.

#### b) RNA isolation

Polyadenylated RNA was isolated from mesangial cells using the Microfast Track (Microfast Track is a Trade Mark) kit (Invitrogen). Total RNA was isolated from glomeruli using RNazol solution (TEL-test Inc.).

#### c) Suppression subtractive hybridisation (SSH)

SSH was performed with the PCR-SELECT cDNA subtraction kit (Clontech) as directed by the manufacturer with the modification that a four-fold greater than recommended amount of driver cDNA was

In Table 1<sup>a</sup> refers to the sequence identity based on comparisons with the Genbank/EMBL database;

<sup>b</sup> refers to an estimate of the size (kb) of the mRNA identified by Northern Blot analysis; and

<sup>c</sup> refers to the differential expression of each gene based on Northern Blot analysis of primary human mesangial cells cultured under indicated conditions relative to expression in cells cultured in 5 mM glucose. Values were obtained by Phosphor-Imaging and were normalised by comparison with glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (\*, detected in mesangial cells cultured in 5 mM glucose + 25 mM mannitol and 30 mM glucose, but not in 5 mM glucose, fold expression is degree of expression relative to that found in 5 mM glucose).

Table 1

Summary of cDNAs identified by SSH as being induced in mesangial cells cultured in high glucose.

Gene <sup>a</sup>	mRNA <sup>b</sup>	Differential Expression <sup>c</sup>	
		30mM glucose	25mM mannitol + 5mM glucose
Extracellular Matrix Proteins			
Fibronectin	7.0	2.1-fold	1.5-fold
Thrombospondin	6.0	7.0-fold	8.0-fold
Actin-Binding Proteins			
MRLC	0.9	3.9-fold	1.6-fold
T-plastin	1.2	4.2-fold	1.8-fold
Caldesmon	3.6	3.3-fold	2.8-fold
Profilin	1.0	2.2-fold	2.3-fold
CAP	2.6	1.5-fold	1.7-fold
ARP3	2.5	2.0-fold	1.0-fold
Growth Factors			
CTGF	2.4	3.0-fold	1.5-fold
Others			
PAI-1	2.0	1.2-fold	1.0-fold
	3.0	3.9-fold	2.0-fold
RBM3	1.5	1.8-fold	1.4-fold
Ubiquitin	3.0	2.3-fold	1.7-fold
TCTP	0.8	4.3-fold	2.5-fold
IHG-1	3.4	*	*
IHG-2	2.5	2.0-fold	2.0-fold

Within a diabetic milieu, high glucose levels may perturb cellular function through glucose-specific actions or by increasing the osmolarity of extracellular fluids. The role of hyperosmolarity as a mediator of gene induction by high glucose was assessed by comparing mRNA levels, as determined by Northern Blot, in cells cultured in either

Within a diabetic milieu, high glucose levels may perturb cellular function through glucose-specific actions or by increasing the osmolarity of extracellular fluids. The role of hyperosmolarity as a mediator of gene induction by high glucose was assessed by comparing mRNA levels, as determined by Northern Blot, in cells cultured in either

30 mM glucose or in 5 mM glucose supplemented with 25 mM mannitol. High glucose was more effective than high osmolarity at inducing expression of CTGF, myosin regulatory light chain (MRLC), actin related protein 3 (ARP3), T-plastin and translationally controlled tumor protein (TCTP). High glucose and mannitol-induced hyperosmolarity afforded equivalent induction of the other products.

### Example 2

#### CTGF expression in mesangial cells cultured in high glucose.

##### a) Influence of high ambient glucose on CTGF mRNA levels in human mesangial cells.

CTGF, is a 38kD cysteine-rich secreted peptide known to modulate ECM production in some extrarenal cell types. In Example 1, SSH analysis identified a cDNA fragment of 250 bp which was identical to bases 814-1061 of the human CTGF cDNA. Induction of CTGF mRNA expression in primary human mesangial cells cultured in high glucose was investigated by Northern Blotting as shown in Fig. 1.

In Fig. 1 the lanes represent the following:

Lane 1: RNA from mesangial cells exposed to 5 mM glucose;

Lane 2: RNA from mesangial cells exposed to 5 mM glucose and 25 mM mannitol;



Lane 3: RNA from mesangial cells exposed to 30 mM glucose for seven days.

5 A 2.4 kb band was detected following hybridisation with the CTGF probe. The relative amounts of CTGF mRNA as estimated by Phosphor Imager quantification are indicated in Fig. 2. All of the values were normalised to GAPDH levels and the results are representative of three independent experiments.

10 The results indicate that CTGF mRNA expression was between 2.5-3.3-fold higher in mesangial cells cultured in 30 mM glucose as compared with 5 mM glucose.

15 b) Effect of CTGF on mesangial cell matrix production.

To investigate the direct effects of CTGF up-regulation on matrix production, in particular the effect on collagens I and IV and fibronectin, mesangial cells were incubated with recombinant CTGF  
20 protein.

Mesangial cells were serum starved for 24 hr in RPMI 1640 medium supplemented with 0.5 % fetal bovine serum (FBS) and then exposed to rhCTGF (8 ng/ml) (a generous gift from Dr. Gary  
25 Grotendorst) for 24 hr (Kreisberg, J.I. and Ayo, S.H. (1993). *Kidney Int.* 43, 109-113). Total RNA was extracted and chromosomal DNA was removed using DNase I (Gibco-BRL). Equal amounts of cDNA were

subsequently amplified by PCR using specific primers for GAPDH  
(Gen/EMBL accession no. AJ005371, sense:

ACCACAGTCCATGCCATCAC (SEQ ID NO: 7); antisense:

TCCACCACCCTGTTGCTGTA (SEQ ID NO: 8), Collagen I

5 (Gen/EMBL accession no. X55525, sense:

GGTCTTCCTGGCTTAAAGGG (SEQ ID NO: 9); antisense:

GCTGGTCAGCCCTGTAGAAG (SEQ ID NO: 10)), Collagen IV

(Gen/EMBL accession no. M11315, sense:

CCAGGAGTTCCAGGATTTCA (SEQ ID NO: 11); antisense:

10 TTTTGGTCCCAGAAGGACAC (SEQ ID NO: 12) and fibronectin

(Gen/EMBL accession no. X02761, sense:

CGAAATCACAGCCAGTAG (SEQ ID NO. 13), antisense:

ATCACATCCACACGGTAG (SEQ ID NO: 14)).

15 Fig. 3 depicts ethidium-stained panels of a 2% (w/v) agarose gel  
containing 10 µl of each PCR reaction after electrophoresis.

In Fig. 3 the lanes represent the following:

20 Lane 1: RT-PCR products from mesangial cells cultured in  
RPMI 1640 and 0.5% FBS;

Lane 2: RT-PCR products from mesangial cells exposed to  
rhCTGF (8 ng/ml) for 24 hr.

These results indicate that rhCTGF up-regulates mesangial cell collagens I and IV and fibronectin. These proteins typify matrix accumulation as seen in diabetic nephropathy.

5 CTGF is a member of a small family of highly homologous proteins termed the CCN family (for CTGF / fisp-12, cefl0/cyr61 and Nov) (Bork, P (1993). *FEBS Letts.* 327, 125-130.). These peptides are characterised by conservation of 38 cysteine residues that constitute more than 10 % of the amino acid content. All members have signal  
10 peptides and appear to be secreted *via* orthodox secretory pathways (Bradham, D.M., (1991) *J. Cell. Biol.* 114, 1285-1294). In the context of diabetic nephropathy, it is intriguing that CTGF which is up-regulated in the presence of ambient glucose, in turn, up-regulates the production of extracellular matrix (ECM). These data demonstrate the potential of  
15 CTGF as a stimulus for increased ECM synthesis and mesangial expansion in diabetic nephropathy.

### Example 3

20 Enhanced CTGF expression in renal cortex and isolated glomeruli of rats with STZ-induced diabetic nephropathy.

To assess CTGF expression in diabetic nephropathy *in vivo*, CTGF mRNA levels were measured in RNA isolated from the cortex of  
25 rats with STZ-induced diabetes mellitus. To this end, PCR primers for rat CTGF were designed from the sequence of the mouse CTGF homologue, fisp12 (Genbank/EMBL accession no. M70642, sense:

CTAAGACCTGTGGAATGGGC (SEQ ID NO: 15); antisense:  
CTCAAAGATGTCATTGTCCCC (SEQ ID NO: 16)) (Ryseck, R.P.,  
(1991) *Cell Growth Differ.* 2, 225-233).

5 RT-PCR was performed on total RNA extracted from renal  
cortex of STZ-diabetic rats and age matched controls. The sequence of  
the rat CTGF transcript was 94 % identical at the nucleotide level (Fig.  
4) and 99 % identical at the amino acid level (Fig. 5) to the mouse  
CTGF homologue fisp12 (bases 783-1123, accession no. M70642).  
10 Nucleotides that differ between the two species are given in upper case  
and the single different amino acid is in bold.

Induction of CTGF mRNA was observed in the renal cortex of  
rats with STZ-induced diabetic nephropathy at four months after  
15 administration of STZ, coincident with mesangial expansion and  
proteinuria as shown in Fig. 6 and data not shown.

Fig. 6 depicts ethidium-stained panels of a 2 % (w/v) agarose gel  
containing 10 µl of each PCR reaction after electrophoresis. CTGF and  
20 GAPDH mRNA levels were analysed in total RNA purified from 2  
diabetic animals with established nephropathy after four months of  
diabetes (lanes 1 and 2) and two age matched control animals (lanes 3  
and 4).

25 CTGF expression was further localized to glomeruli by RT-PCR  
analysis of RNA extracted from glomeruli isolated by differential  
sieving from the renal cortex of rats with STZ-induced diabetic

nephropathy. Glomerular levels of CTGF mRNA were increased by 2.5-fold and 1.6-fold after two months and four months of diabetes, respectively, by comparison with age and sex-matched controls. The significance of these observations is further supported by a recent report demonstrating CTGF expression in a screen of human renal diseases including diabetic nephropathy (Ito, Y., *et al.* (1998) *Kidney Int.* 53, 853-861).

#### Example 4

#### 10     Induction of mesangial cell CTGF expression by high glucose involves           TGF- $\beta$ 1 dependent and independent pathways.

It has been shown that TGF-  $\beta$ 1 is a stimulus for mesangial matrix accumulation in diabetic nephropathy. In our experimental model as described in Example 1, high glucose concentrations provoked induction of TGF- $\beta$ 1 mRNA expression in cultured human mesangial cells over the same temporal framework as CTGF expression (data not shown).

20           To assess the role of TGF- $\beta$ 1 as a stimulus for CTGF expression in response to high glucose, cells were incubated in either 5 mM glucose or 30 mM glucose plus 1  $\mu$ l/ml anti-TGF- $\beta$ 1 antibody for seven days with three changes of medium. Cells were serum starved for 24 hr in RPMI 1640 and 0.5% FBS. 10 ng/ml TGF- $\beta$ 1 (Calbiochem) or 10  
25   ng/ml TGF- $\beta$ 1 preadsorbed with 1  $\mu$ g/ml neutralising anti-TGF- $\beta$ 1 polyclonal antibody were subsequently added for 24 hr.

The role of PKC on CTGF expression in response to high glucose was investigated by culturing the mesangial cells in either 5 mM, 30 mM glucose or 30 mM glucose and the PKC inhibitor GF 102903X.

5

Fig. 7 is an autoradiograph of CTGF mRNA levels analysed by Northern Blot and depicts the results obtained when mesangial cells were exposed to TGF- $\beta$ 1 (10 ng/ml) for 24 hr in the presence (lane 3) and absence (lane 2) of anti-TGF- $\beta$ 1 neutralising antibody (1  $\mu$ g/ml).

10 Cells cultured in RPMI 1640 and 0.5 % FBS for 24 hr served as control (lane 1). A 2.4 kb band was detected following hybridisation to the CTGF probe. The blot was stripped and reprobed with GAPDH. The relative amount of CTGF mRNA as estimated by Phosphor Imager quantification (Fig. 8). Values were normalised to GAPDH levels and  
15 the results are representative of two independent experiments.

These results indicate that TGF- $\beta$ 1 is a potent inducer of increased CTGF mRNA levels under these conditions. This effect was inhibited by the addition of a neutralising anti-TGF- $\beta$ 1 antibody as  
20 depicted in Fig. 7.

Fig. 9 is an autoradiograph of CTGF mRNA levels analysed by Northern Blot and depicts the results obtained when mesangial cells were exposed to 5 mM glucose (lane 1), 30 mM glucose (lane 2) and 30 mM glucose in the presence of anti-TGF- $\beta$ 1 neutralising antibodies (1  $\mu$ g/ml) (lane 3) for seven days. A 2.4 kb band was detected following hybridisation to the CTGF probe. The blot was stripped and probed with  
25

GAPDH. The relative amount of CTGF mRNA as estimated by Phosphor Imager quantification (Fig. 10). Values were normalised to GAPDH levels.

5           The neutralising anti-TGF- $\beta$ 1 antibody partially attenuated the glucose-induced increase in CTGF transcript level in mesangial cells grown in 30 mM glucose for 7 days (Fig. 9), suggesting that high glucose triggers mesangial cell CTGF expression through TGF- $\beta$ 1-dependent and independent pathways.

10

          Fig. 11 is an autoradiograph of CTGF mRNA levels analysed by Northern Blot and depicts the results obtained when mesangial cells were exposed to 5 mM glucose (lane 1), 30 mM glucose (lane 2) and 30 mM glucose in PKC inhibitor GF102903X (10  $\mu$ M) (lane 3) for four  
15       days. A 2.4 kb band was detected following hybridisation to the CTGF probe. The blot was stripped and probed with GAPDH. The relative amount of CTGF mRNA as estimated by Phosphor Imager  
          quantification (Fig. 12). Values were normalised to GAPDH levels.

20

          Whereas the PKC inhibitor GF102903X was without effect on TGF- $\beta$ 1-induced CTGF expression in our system (data not shown), this compound afforded partial inhibition of high glucose-induced CTGF expression (Fig. 11).

25

          CTGF shares some of the biological actions of TGF- $\beta$ 1 such as stimulation of cell proliferation and extracellular matrix protein synthesis in fibroblasts. When considered in this context, our results

suggest that TGF- $\beta$ 1 may promote mesangial matrix production, in part, by inducing CTGF synthesis. TGF- $\beta$ 1 has a complex profile of biological activities that includes pro-inflammatory, pro-fibrotic and anti-inflammatory effects. By targeting CTGF it may be possible to attenuate the sclerosis-inducing effects of TGF- $\beta$ 1 while preserving its more desirable anti-inflammatory activities.

### Example 5

10

#### Further characterisation of IHG-2

15

20

25

IHG-2 is a mesangial cell gene which we have identified as being induced in human mesangial cells by high extracellular glucose as described in Example 1. To further characterise this gene, IHG-2 was searched against the dbEST using the BLAST algorithm. This search identified a clone that was 94 % identical to ESTAA071138, clone no: 530117 3'. The sequence for the 5' end of this clone was also in the database, which again identified multiple ESTs. These ESTs showed homology with the 3' untranslated region (UTR) of a rat cDNA clone known as drm/Gremlin. As indicated above, gremlin/drm, together with DAN and cerberus, are members of the cysteine knot super-family which includes TGF $\beta$  and bone morphogenetic protein (BMP). A second EST W48852, clone no:324951 3', was identified from the IHG-2 BLAST. The 5' end of this clone, EST W48619, was also searched against the database, from which EST AA373348 was obtained. This clone showed homology with the drm 3' UTR, approximately 500 bp from the open reading frame (ORF). Thus, it was possible to make a



direct link from IHG-2 to within 500 bp of the ORF of *drm/gremlin*. Therefore, by establishing a link between EST AA37348 and the ORF of *drm/gremlin*, it was confirmed that IHG-2 is part of the 3' UTR of this gene. Primers were designed to recognise the ORF, IHG-2, and the EST clone AA373348. An initial PCR using primers corresponding to the start site of the *gremlin/drm* gene together with a primer within the IHG-2 clone would give a predicted product of approximately 2.5 kb. This product was nested with primers corresponding to the 3' end of the ORF of *gremlin* and the EST clone AA373348, generating a product of approximately 500 bp, thus verifying that this EST is in the UTR of the human *drm/gremlin* gene. Therefore, IHG-2 was found to be part of the *drm/gremlin* gene, which was not previously known (Fig. 13).

#### Example 6

Use of cloning *in-silico* coupled with PCR to demonstrate that IHG-2 is part of the 3' untranslated region of *gremlin*

In Example 5 we describe the identification of a transcript, IHG-2, the sequence of which did not show homology against the cumulative database of characterised sequences using the BLAST algorithm.

Bioinformatic analysis was carried out as follows:

Database searching and alignments were performed at the National Center for Biotechnology Information (NCBI) Bethesda, Maryland, U.S.A. using the Basic Local Alignment Search Tool

Algorithm (BLAST) (Altschul, S.F., *et al.* (1997) *Nucleic Acids Res.* 25, 3389-3402). The Non Redundant (nr) and the Expressed Sequence Tag (EST) databases were sourced. Contiguous sequences were generated using Fragment Assembly, a program within the Genetics Computer Group Inc. package. UniBlast (Guffanti, A., and Simon, G., *Trends in Genetics*, 14, 293) was used to identify homologous clusters within the UniGene database and to verify the consensus sequence derived from ESTs. Chromosomal localization data were obtained from the UniGene and Online Mendelian Inheritance in Man (OMIM) databases.

10

To further characterise the sequence, the sequence of IHG was searched against the EST database where a number of matches were obtained. Each of these matches was, in turn, searched against the nr database at NCBI. Four ESTs, namely W52686, N28395, H80042, and W47324, showed low homology to the 3' UT region of the rat gene *drm* referred to in Example 5. The ORF of the human homologue of this gene, *gremlin*, was also in the database.

15

To generate a link between the ORF of *gremlin* and IHG-2, successive BLAST searches were used to identify overlapping sequences in the EST database.

20

However, it was not possible to directly link IHG-2 to the ORF of *gremlin* with sequences within the EST database. Therefore, RNA isolated from human mesangial cells was reverse transcribed with a primer that recognises IHG-2. PCR analyses were performed spanning the regions shown in Fig. 13.

25

In this graphical representation of a BLAST output from the EST database, the thick bar of 4 kb represents the final composite sequence of the gremlin gene. Each of the other bars represents an individual sequence, in the EST database, that were assembled, where possible, into continuous sequences, and demonstrates how cloning *in-silico* was used to generate the contiguous sequence. The region of no EST overlap was generated by reverse transcription of human mesangial mRNA with a complementary primer to IHG-2. PCR was performed spanning the regions indicated (by arrows), and the resulting products were sequenced, allowing a contiguous cDNA of 4049 bp to be generated which included the open reading frame of gremlin and IHG-2.

Human gremlin and rat drm cDNAs were compared and Fig. 14 shows a graphical representation of an alignment between rat drm and human gremlin together with the region corresponding to IHG-2 using the BLAST algorithm. Sequence homology was found to be high in the coding region of the cDNA; however, there are only small regions of homology within the 3' UT region. This explains why IHG-2 did not identify drm in a BLAST search, but a match to drm, and thus gremlin, was obtained by examining EST sequences further. The lack of homology between rat drm and human gremlin probably results from decreased selective pressure on the 3' UT region of gene homologues to remain the same between species.

Fig. 15 shows the final sequence of human mesangial cell gremlin, indicating the ORF and the region corresponding to IHG-2

(GenBank accession no: AF110137). Shown are the 5' and 3' UT sequence, and the open reading frame (with translation). The boxed region corresponds to the location of IHG-2. At the time of submission, this sequence matched 136 separate EST entries in the EST database. Of these entries, 23.5% were derived from fibroblast libraries; 30% were from bone tissue libraries; and 34% were derived from tumor related libraries. The sequence was also searched against the UniGene database using the UniBlast program. This identified 4 UniGene clusters, Hs.214148, Hs.40098, Hs.114330, and Hs.239507. Two of these clusters, Hs.40098, and Hs.239507, have been mapped to intervals D15S118-144 and D15S144-165 on chromosome 15, respectively. Secretory granule neuroendocrine protein 1 and the alpha polypeptide of the nicotinic cholinergic receptor have been mapped to either side of these clusters and have also been mapped more specifically to the 15q11-15 interval. Analysis of the OMIM database reveals that the formin gene, which was recently shown to induce gremlin expression in the developing limb bud (Zuniga, A., *et al.* (1999) *supra* ), is also localised to this interval. Diabetes mellitus with multiple epiphyseal dysplasia, or Wolcott-Rallison syndrome, is localised to the 15q11-12 interval (Stewart, F.J., *et al.*, (1996) *Clin. Genet.* 49, 152-5). In the epiphyseal growth plate, immunohistochemical studies have revealed that BMP-2 and 4 are expressed in proliferating and maturing chondrocytes, suggesting that BMP and its receptors play roles in the multi-step cascade of enchondral ossification (Yazaki, Y., *et al.*, (1998) *Anticancer Res.* 18, 2339-44). Regulation of gremlin expression may have implications in both of the disease states associated with Wolcott-Rallison syndrome.

Example 7Induction of mesangial cell gremlin expression *in vitro* by high glucose  
and cyclic mechanical strain induce

A) Primary cultures of human mesangial cells were propagated as described in Example 1, except that the medium was supplemented with 5% FBS. Treatment of cultures with glucose was carried out as described in Example 1. Mesangial cells were exposed to either 5m M glucose or 30mM glucose for seven days.

Northern Blot analysis as described further below was performed on RNA extracted from mesangial cells grown in either 5 mM ('normal') or 30 mM ('high') glucose using the ORF of gremlin and IHG-2 probes. Both probes detected a 2-fold increase in gene expression under high glucose conditions as depicted in Fig. 16.

All subsequent northern analysis was performed using the ORF of gremlin as a probe.

Northern Blots were performed using formaldehyde denaturation according to standard protocols and quantitated using a phosphorimager (Biorad). PCR products used to generate the probes for northern analysis were amplified using primers for the open reading frame (ORF) of gremlin (sense: ATGAGCCGCACAGCCTACAC (SEQ ID NO: 17); antisense TTAATCCAAATCGATGGATATGC (SEQ ID NO: 18)), and

for IHG-2 (sense: CTCAGCCTCCTAGCCAAGTCC (SEQ ID NO 19); antisense: GTATTGTCCACATTCTCCAAC (SEQ ID NO: 20)).

Fibronectin and GAPDH probes were generated as described in Example 2

5 Specific primers were used to amplify gremlin/IHG-2 (external sense: ATGAGCCGCACAGCCTACAC (SEQ ID NO: 21); external antisense: GTATTGTCCACATTCTCCAAC (SEQ ID NO: 22); internal sense: GAGAGTCACACGTGTGAAGC (SEQ ID NO: 23); internal antisense: AGGAGGATGCAAGCACAGG (SEQ ID NO: 24), BMP-2 (external  
10 sense: CGCGGATCCTGCTTCTTAGACGGACTGCG (SEQ ID NO: 25); external antisense: TTTGCTGTACTAGCGACACC (SEQ ID NO: 26); internal sense: CAAGATGAACACAGCTGG (SEQ ID NO 27)), and GCTCAGGATACTCAAGAC (SEQ ID NO: 28)). RT-PCR was carried out as reported as described in Example 3.

15

The results are shown in Figs. 16 and 17.

In Figs. 16 and 17, lane 1 corresponds to the mesangial cells exposed to 5 mM glucose and lane 2 corresponds to the mesangial cells  
20 exposed to 30 mM glucose.

Fig. 16 is an autoradiograph of IHG-2 (1), gremlin (2), fibronectin (3) and GAPDH (4) mRNA levels analysed by Northern Blot. Two bands of approximately 4.4 kb and 4.6 kb were detected  
25 following hybridisation to the gremlin and IHG-2 probes.

Fig. 17 depicts relative mRNA levels as estimated by Phosphor Imager quantification. Values were normalised to GAPDH levels. The results are representative of three independent experiments.

5 B) Glomerular hypertension is an independent risk factor for the development of glomerulosclerosis in diabetes mellitus (Brenner, B.M., *et al.* (1982) *N. Engl. J. Med.* 307, 652-9). To model the effects of glomerular hypertension on mesangial cell gremlin expression in the present study, mesangial cells were propagated under conditions of  
10 cyclic mechanical strain for 24 and 48 h in the Flexercell™ System

For the application of mechanical cyclic stretch, primary human mesangial cells were seeded on either flexible or rigid based, elastin coated six-well plates (Flex I and Flex II plates, Flex Cell™ Int,  
15 Hillsborough, NH, USA). Cells were grown to 90% confluency, then serum restricted in Clonetics™ Mesangial Basal Medium supplemented with 0.5% fetal calf serum. Cells cultured on flexible plates were subjected to repeated cycles of computer-controlled, vacuum-driven mechanical stretch and relaxation using the Flexercell Strain Unit FX-  
20 2000 (Flexercell™). Cells were alternately stretched and relaxed at 0.5 sec intervals (60 cycles/min) for either 24 or 48 h. The applied vacuum achieved a 17% elongation of the outer annulus of the culture plates. All experiments were carried out at 37°C and 5% CO<sub>2</sub> in a humidified incubator.

The results were obtained from three diabetic rats, 14 weeks following onset of diabetes and from three age matched controls.

5 The model used perturbs mesangial cell matrix production and metabolism in a manner similar to that observed in diabetic glomerulosclerosis *in vivo*. Mesangial cell gremlin mRNA levels were significantly enhanced under conditions of mechanical strain, in parallel with increased fibronectin mRNA expression as shown in Figs. 18 and 19.

10

Referring to Figs. 18 and 19 mesangial cells in culture were grown under static conditions (lane 1) or during exposure to cyclic stretch for 24 h (lane 2) or 48 h (lane 3) using the Flexercell™ System.

15

Fig. 18 is an autoradiograph of gremlin(1), fibronectin(2) and GAPDH(3) mRNA analysed by Northern Blot.

In Fig. 18 the lanes represent the following:

Lane 1: Mesangial cells grown in culture under static conditions;

20

Lane 2: Mesangial cells grown in culture during exposure to cyclic stretch for 24 h; and

Lane 3: Mesangial cells grown in culture during exposure to cyclic stretch for 48 h.

25

Fig. 19 depicts relative mRNA levels as estimated by Phosphor Imager quantification. Values were normalised to GAPDH levels.



To assess gremlin expression in diabetic nephropathy *in vivo*, gremlin mRNA levels were measured by Northern Blot analysis with RNA isolated from the renal cortex of control rats and from diabetic rats 14 weeks after induction of diabetes mellitus by streptozotocin (STZ).

5 In keeping with the *in vitro* experiments reported above, gremlin mRNA levels were increased in kidneys from diabetic rats, coincident with proteinuria and histologic evidence of diabetic nephropathy (data not shown).

10 Nine Male Munich-Wistar uninephrectomized rats were rendered diabetic with streptozotocin, and the RNA extracted as described in Example 3.

The results are shown in Figs. 20 and 21, which show gremlin  
15 mRNA levels in renal cortex of STZ-diabetic rats.

Fig. 20 is an autoradiograph of gremlin mRNA levels in the kidney cortex of a STZ-diabetic rat (lane 2) and an age matched control (lane 1) analysed by Northern Blot. A band of approximately 4.4kb was  
20 detected following hybridisation to the gremlin probe.

Fig. 21 depicts relative mRNA levels as estimated by Phosphor Imager quantification. Values were normalised to GAPDH levels.

Example 8Regulation of mesangial cell gremlin expression by high glucose:  
evidence for involvement of TGF- $\beta$ 1

5

As indicated above, both high ambient glucose concentrations and cyclic mechanical strain provoke TGF- $\beta$ 1 production by mesangial cells *in vitro* and TGF- $\beta$ 1 appears to be a major stimulus for mesangial matrix accumulation in diabetic glomeruli *in vivo*. To probe the mechanism by which high glucose triggers gremlin expression, primary human mesangial cells were propagated in 5 mM or 30 mM glucose in the presence and absence of anti-TGF- $\beta$ 1 neutralising antibody (1  $\mu$ g/ml). Treatment of cultures with glucose and anti-TGF- $\beta$ 1 were as described in Example 1 and Example 4, respectively. To assess the role of TGF- $\beta$ 1 as a stimulus for gremlin expression, cells were serum restricted for 24 h in MCDB131 and 0.5% PBS and subsequently treated with 10ng/ml TGF- $\beta$ 1. MCDB131 is a specialised medium for the growth of mesangial cells and is obtained from Clonetics.

20

Initial studies had indicated that TGF- $\beta$ 1 neutralizing antibody (data not shown) blunted glucose-triggered gremlin expression and therefore the ability of TGF- $\beta$ 1 to alter gremlin expression was investigated. The results are shown in Figs. 22 and 23.

25

The addition of exogenous human recombinant TGF- $\beta$ 1 (10 ng/ml, 24 h) to serum restricted (24 h) mesangial cells also augmented

gremlin mRNA levels, suggesting that high glucose enhances gremlin mRNA expression, at least in part, through its ability to stimulate TGF- $\beta$ 1 expression. In aggregate, these observations suggest the presence of a novel autocrine loop through which TGF- $\beta$ 1 induces gremlin gene expression and may thereby regulate the activity of mesangial-derived BMPs as hereinafter described.

It was found that gremlin expression in response to high glucose (30 mM, 7 days) was reduced in the presence of anti-TGF- $\beta$ 1 antibody (data not shown). To further probe the role of TGF- $\beta$ 1 as a modulator of gremlin expression, mesangial cells were exposed to TGF- $\beta$ 1 (10 ng/ml) for 24 h (lane 2). Cells cultured in MCDB131 and 0.5% FBS for 24 h served as a control (lane 1).

Fig. 22 is an autoradiograph of gremlin (1), fibronectin (2) and GAPDH (3) mRNA levels analysed by Northern Blot.

Fig. 23 shows relative mRNA levels as estimated by Phosphor Imager quantification. Values were normalised to GAPDH levels.

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Whereas little or no BMP-2 mRNA was detected in mesangial cells propagated in 5 mM glucose, a marked induction of BMP-2 expression was observed in cells cultured in 30 mM glucose as shown in Fig. 24.

5

In contrast, BMP-4 expression levels were relatively unchanged. Interestingly, whereas BMP-2 does not stimulate fibronectin expression in mesangial cells *in vitro*, BMP-2 has been recently shown to block mesangial cell proliferation triggered by epidermal growth factor and platelet-derived growth factor (Ghosh Choudhury, G., *et al.*, (1999) *J. Biol. Chem.* 274, 10897-902; Ghosh Choudhury, G., *et al.*, (1999) *Biochem. Biophys. Res. Commun.* 258, 490-6). Our results raise the possibility that TGF- $\beta$ 1 stimulated expression of gremlin may contribute to mesangial cell proliferative responses in this setting. The influence of gremlin on cell proliferation appears complex, however, and may vary markedly depending on the cell-type and proliferative stimulus. In contrast to the aforementioned potentially pro-proliferative actions, over-expression of the gremlin homologue, *drm*, causes apoptosis in fibroblasts by an ERK mediated pathway, while cells transformed with oncogenes such as *v-mos* show suppressed *drm* expression (Topol, L.Z., *et al.*, (1997) *Mol. Cell. Biol.* 17, 4801-10 ). Similarly, over-expression of DAN, another cysteine knot super-family member with homology to *drm*/gremlin, retards fibroblast entry into S phase (Ozaki, T., *et al.*, (1995) *Cancer Res.* 55, 895-900 ).

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In summary, our results demonstrate that the DAN family member gremlin is induced in diabetic nephropathy *in vivo* and implicate both metabolic and hemodynamic stress as stimuli for gremlin expression.

5           The findings that high glucose-triggered gremlin expression is mimicked by addition of exogenous TGF- $\beta$ 1, blunted by anti-TGF- $\beta$ 1 neutralising antibody, and occurs in association with induction of mesangial cell BMP-2 suggests the presence of a novel autocrine loop which may limit the bioactivity of TGF- $\beta$ 1 superfamily members and  
10          modulate mesangial cell proliferation within the diabetic mesangium. The further elucidation of the functional interactions of the DAN family of secreted proteins, such as gremlin, with TGF- $\beta$ 1 superfamily members may shed light on the complex multi-pronged molecular events that perturb cell proliferation and matrix production in diabetic  
15          glomerulosclerosis.

Claims: -

1. A method for identifying a gene having a role in the presentation  
5 of diabetic nephropathy, which method comprises culturing mesangial  
cells in a medium in the presence of a concentration of glucose  
sufficient to induce differential expression of a gene susceptible to such  
differential expression and identifying the gene so induced by  
suppression subtractive hybridisation.
- 10 2. A method according to Claim 1, wherein the mesangial cells are  
cultured in the presence of a concentration of glucose sufficient to  
induce up-regulation of a gene susceptible to such up-regulation.
- 15 3. A method according to Claim 1 or 2, wherein the concentration  
of glucose is greater than 5 mM.
4. A method according to any preceding claim, wherein the  
mesangial cells are subjected to mechanical strain.
- 20 5. A method according to any preceding claim, wherein  
transforming growth factor  $\beta 1$  (TGF- $\beta 1$ ) is added to the culture  
medium.

6. A method according to any one of Claims 1-5, wherein the possibility of differential expression due to hyperosmolarity is excluded.

5 7. A method according to any one of Claims 1-6, wherein the gene so differentially expressed is a gene which includes a sequence selected from:

10 1) SEQ ID NOS: 1-3;

2) SEQ ID NO: 4;

3) SEQ ID NO: 5; and

15 4) SEQ ID NO: 6.

8. Use of a gene identified by a method according to any one of Claims 1-7, as a diagnostic marker for the progression and presentation of diabetic nephropathy.

20

9. Use of a gene identified by a method according to any of Claims 1-7, as an index of disease activity and the rate of progression of diabetic nephropathy.

25 10. Use of a gene identified by a method according to any of Claims 1-7, as a basis for identifying drugs for use in the prevention and/or therapy of diabetic nephropathy.



11. A sequence selected from any one of SEQ ID NOS: 1-3, 5 and 6 according to Claim 7.

5

PCT

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<p>(21) International Application Number: PCT/IE00/00026 (22) International Filing Date: 28 February 2000 (28.02.00) (30) Priority Data: 990157 26 February 1999 (26.02.99) IE (71) Applicants (for all designated States except US): HIBERGEN LIMITED [IE/IE]; Cork Airport Business Park, Kinsale Road, County Cork (IE). UNIVERSITY COLLEGE DUBLIN, NATIONAL UNIVERSITY OF IRELAND, DUBLIN [IE/IE]; Belfield, Dublin 4 (IE). (72) Inventors; and (75) Inventors/Applicants (for US only): BRADY, Hugh, Redmond [IE/IE]; "Aspen", Violet Hill, Killiney, County Dublin (IE). GODSON, Catherine, Mary [IE/IE]; 12 Yale, Ardilea, Dublin 14 (IE). MARTIN, Finian, Mary [IE/IE]; 104 Mount Anville Road, Goatstown, Dublin 14 (IE). (74) Agent: ANNE RYAN &amp; CO.; 60 Northumberland Road, Ballsbridge, Dublin 4 (IE).</p>		<p>(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).</p> <p><b>Published</b> <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i></p>
<p>(54) Title: IDENTIFICATION OF GENES HAVING A ROLE IN THE PRESENTATION OF DIABETIC NEPHROPATHY</p>		
<p>(57) Abstract</p> <p>A method for identifying a gene having a role in the presentation of diabetic nephropathy comprises culturing mesangial cells in the presence of a concentration of glucose sufficient to induce differential expression, especially up-regulation, of a gene susceptible to such differential expression and identifying the gene so induced. The cells are also optionally subjected to mechanical strain and/or TGF-<math>\beta</math>1 can be added to the culture medium. The differentially expressed genes can be identified by suppression subtractive hybridisation. The method has resulted in the identification of novel genes which play a role in the presentation of diabetic nephropathy. The genes can be used as diagnostic markers for diabetic nephropathy and as the basis of drug development programmes.</p>		

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Godson, Catherine Mary  
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atttaatgta attattactt caaatccttt ggtcactgtg atttcaagca tgttttcttt 3420  
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aagcaatatt aagaaagact ttaaatgtta ttttgaaga cttacgatgc atgtatacaa 3660  
acgaatagca gataatgat actagttcac acataaagtc cttttaagga gaaaatctaa 3720  
aatgaaaagt ggataaacag aacatttata agtgatcagt taatgcctaa gagtgaaagt 3780  
agttctattg acattctca agatatata tatcaactgc attatgtatt atgtctgctt 3840  
aaatcattta aaaacggcaa agaattatat agactatgag gtaccttgct gtgtaggagg 3900  
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actagaattt aattttcacc ccaataatgt tctatatagc ctttgctaaa gagcaactaa 4020  
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REC'D PCT/PTO 19 DEC 2001

09/914,191

SEQUENCE LISTING



<110> BRADY, Hugh Redmond et al.

<120> Identification of genes having a role in the presentation of diabetic nephropathy

<130> 1377-0170P

<140> US 09/914,191

<141> 2001-08-24

<150> 990157

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gggcttgcac ggttaagcac accagaactg aagcgcaaaa gggtcagctg tcttcactca 300
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gctttgtcct ggtccgggtc actgccatct ttttctcttc catttctgtt ggcagcttaa 420
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tcggcagctc attattatag ttgatgttga attcagaaaa caaatctca ttcttgtctg 540
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tgaggaggyca cgtgagtcac gaactttact ggctcttctt ttaaaccaat tggttttccg 180
cttgwacaca aagctgtact catcactctg tccataacgc gatcacaata tcctctagtt 240
```



*(Musical notation for Example 6)*

```
<210> 6
<211> 309
<212> DNA
<213> Homo sapiens
```

```
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actgacacac ctccatgtgc ccaagcatgg gtttgatcac aggtcacatg cagtttttttg 180
catagtaaatt gtatcattgt tcttttcttc cctcctaaag gaaacagagg aatccacctg 240
tatagagagt ccatgtaggg ataaacttaa aggacagatg acacattggt catgttcgtg 300
ataagagaaa                                     309
```

```
<210> 7
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<212> DNA
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```

```
<400> 7
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```

```
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<400> 8  
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```
<210> 9
<211> 20
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<400> 9  
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```
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<212> DNA
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```

<400> 10  
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*(The following information was obtained from the above-mentioned sources.)*

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```

```
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```

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```

```
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<212> DNA
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```
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<211> 18
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```
<400> 14
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```
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<212> DNA
<213> Homo sapiens
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```
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<211> 21
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<210> 17
<211> 20
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atgatgttca tcaagacctg tgccctgccat tacaactgtc c 341

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atccggacac ctaaaatcgc caagcctgtc aagtttgagc tttctggctg caccagtgtg 180  
aagacataca gggctaagtt ctgcggggtg tgcacagacg gccgtgctg cacaccgcac 240  
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atgatgttca tcaagacctg tgccctgccat tacaactgtc c 341

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<212> PRT  
<213> Rattus sp.

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Gln Ser Arg Leu Cys Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu  
20 25 30  
Asn Ile Lys Lys Gly Lys Lys Cys Ile Arg Thr Pro Lys Ile Ala Lys  
35 40 45  
Pro Val Lys Phe Glu Leu Ser Gly Cys Thr Ser Val Lys Thr Tyr Arg  
50 55 60  
Ala Lys Phe Cys Gly Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His  
65 70 75 80  
Arg Thr Thr Thr Leu Pro Val Glu Phe Lys Cys Pro His Gly Glu Ile  
85 90 95  
Met Lys Lys Asn Met Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn  
100 105 110  
Cys

<210> 32  
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<400> 32

Ile Ser Thr Arg Val Thr Asn Asp Asn Thr Phe Cys Arg Leu Glu Lys  
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 Asn Ile Lys Lys Gly Lys Lys Cys Ile Arg Thr Pro Lys Ile Ala Lys  
 35 40 45  
 Pro Val Lys Phe Glu Leu Ser Gly Cys Thr Ser Val Lys Thr Tyr Arg  
 50 55 60  
 Ala Lys Phe Cys Gly Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His  
 65 70 75 80  
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Cys

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 cctgcatgt gacggagcgc aaatacctga agcgagactg gtgcaaaacc cagccgctta 360  
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 gccagtgcaa ctctttctac atccccaggc acatccggaa ggaggaaagt tcctttcagt 480  
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 ccacgattt ggattaagcc aaatccaggt gcacccagca tgtcctagga atgcagcccc 660  
 aggaagtccc agacctaaaa caaccagatt cttacttggc ttaaacctag aggccagaag 720  
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 ctcacatcta aaggggcggg gccgtggtct ggttctgact ttgtgttttt gtgccctcct 960  
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 ttttgtgaag accctccaga ctctgggaga ggctgggtgt ggcaaggaca agcaggatag 1260  
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 attaactttg gccgttgcaa tctgtctaaa cctaacacca aactgaaaac ataaatactg 1500  
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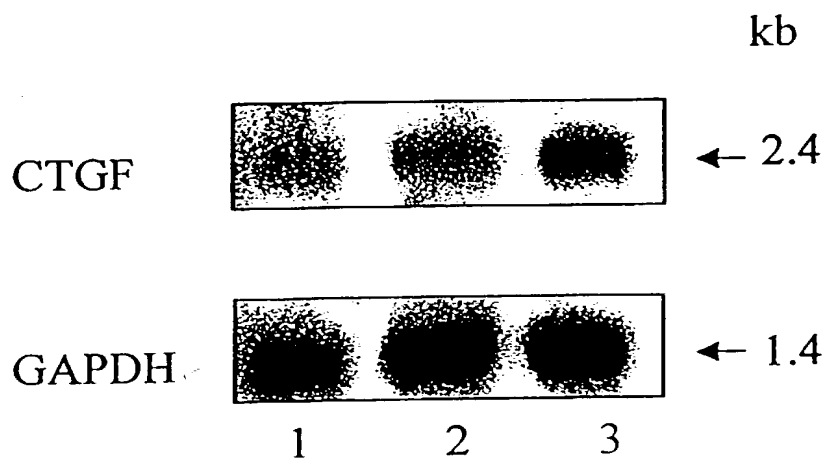


Fig. 1

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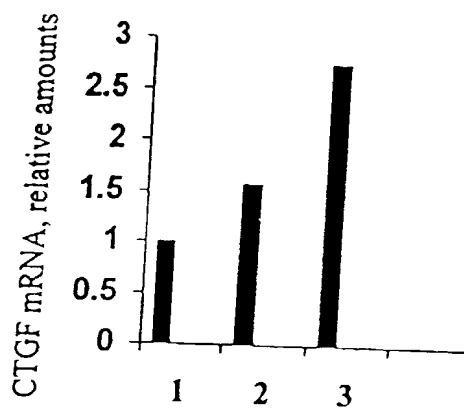


Fig. 2



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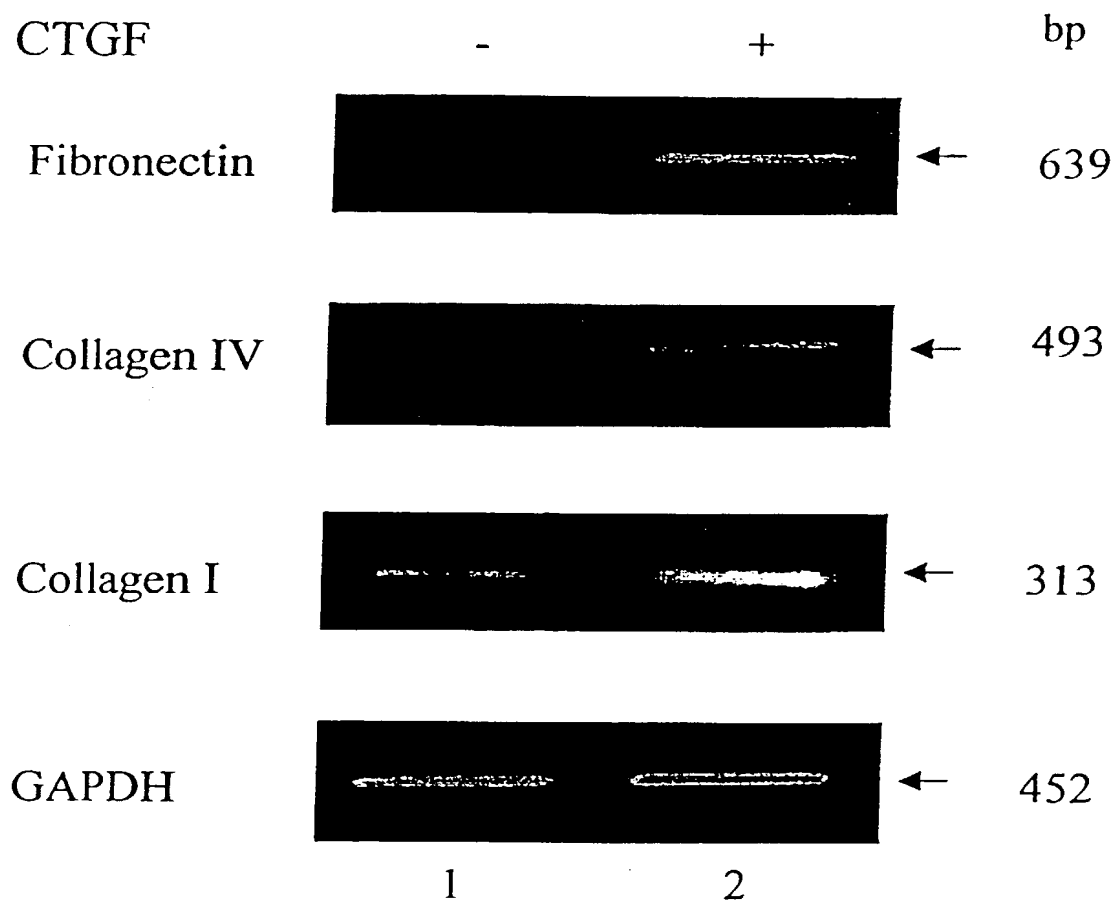


Fig. 3

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[illegible]

Fig. 4

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rat: 1 ISTRVTNDNTFCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKIAKPVKFELSGCTSV 180  
mouse: 216 ISTRVTNDNTFCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKIAKPVKFELSGCTSV 275

rat: 181 KTYRAKFCGVCTDGRCCCTPHRTTTL PVEFKCPHGEIMKKNNMMFIKTCACHYNC 339 (SEQ ID NO: 31)  
mouse: 276 KTYRAKFCGVCTDGRCCCTPHRTTTL PVEFKCPDGEIMKKNNMMFIKTCACHYNC 328 (SEQ ID NO: 32)

Fig. 5

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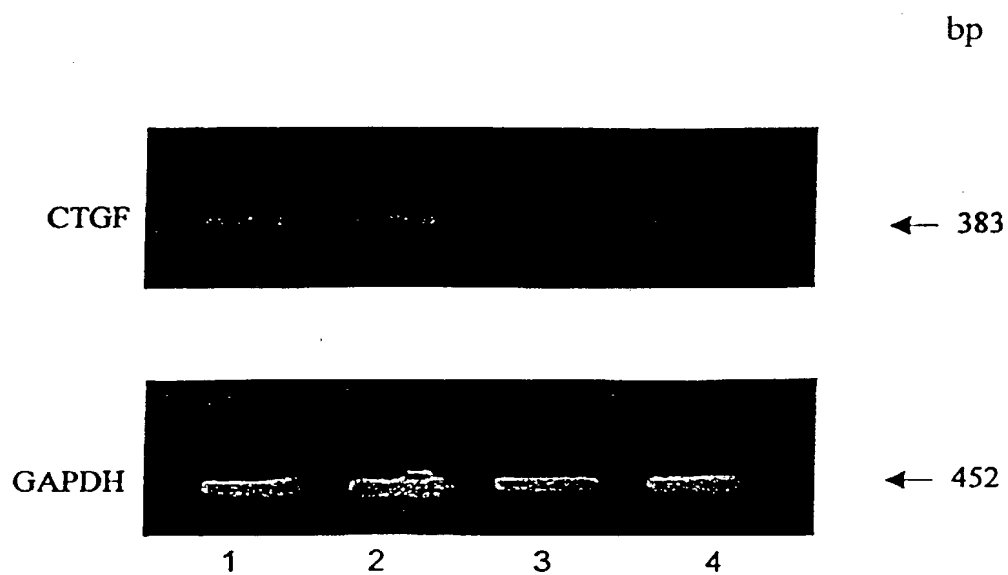


Fig. 6

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PCT/IE00/00026

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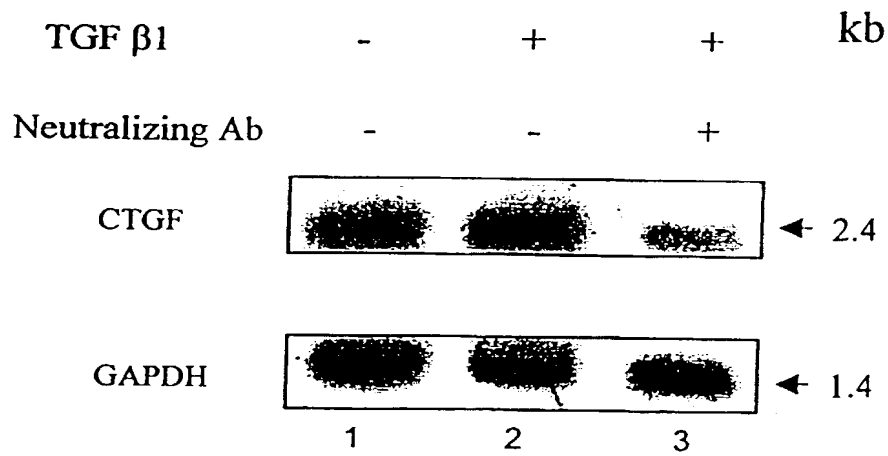


Fig. 7

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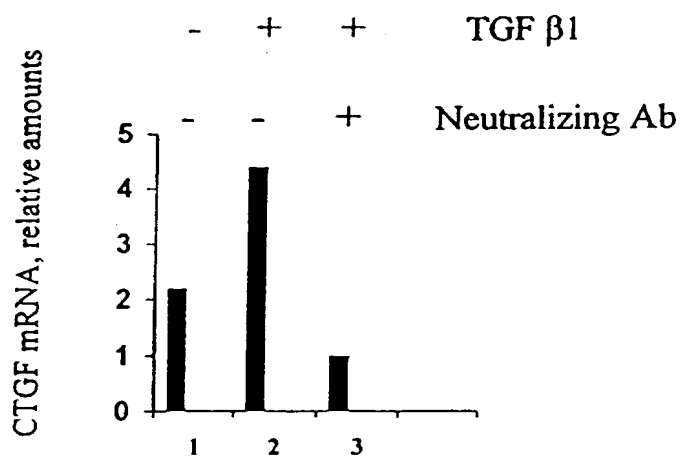


Fig. 8

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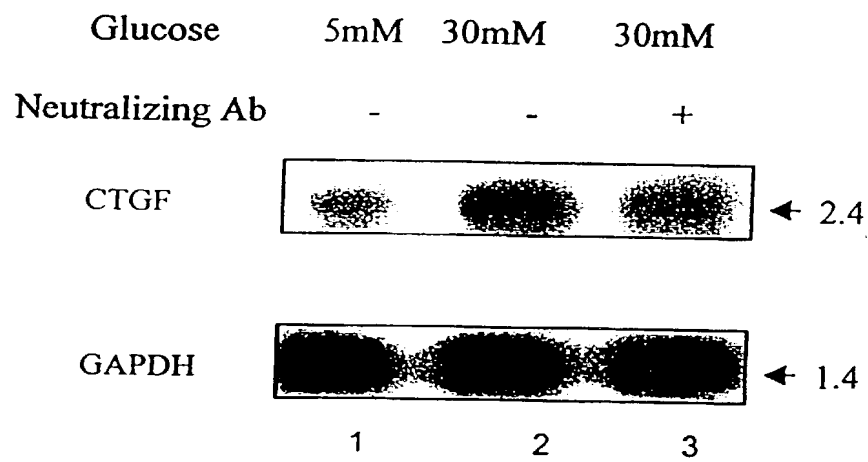


Fig. 9

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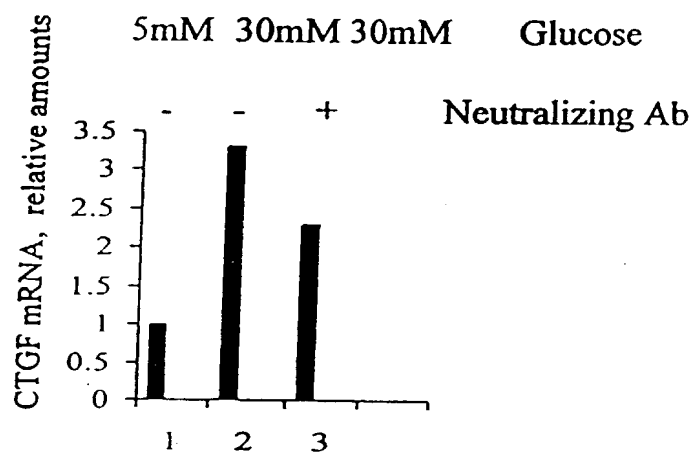


Fig. 10



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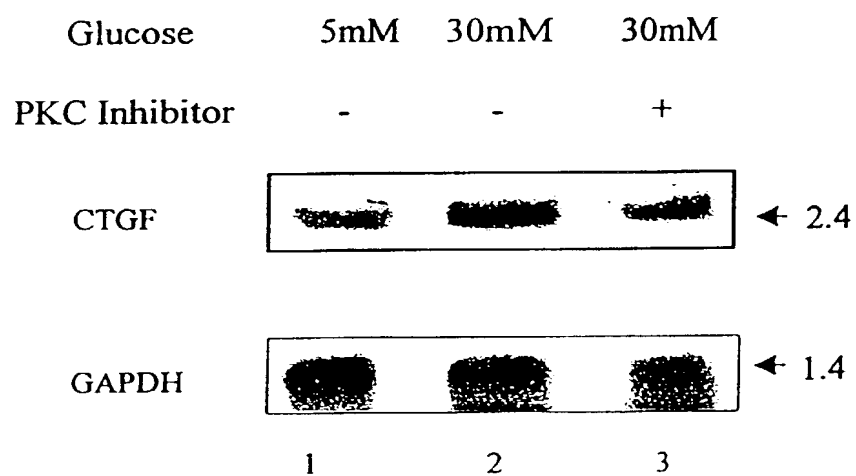


Fig. 11

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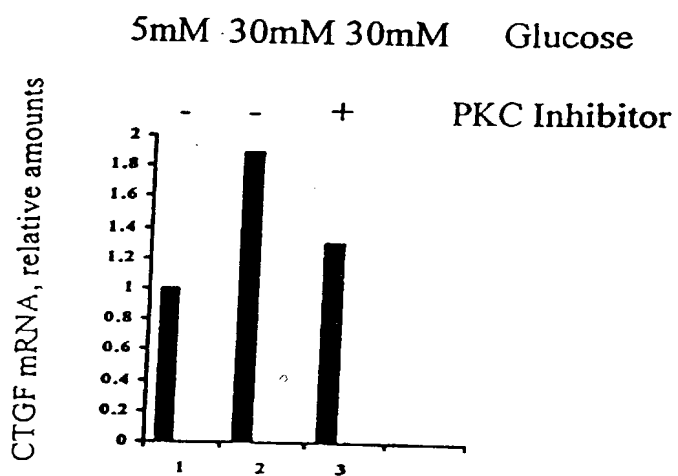


Fig. 12

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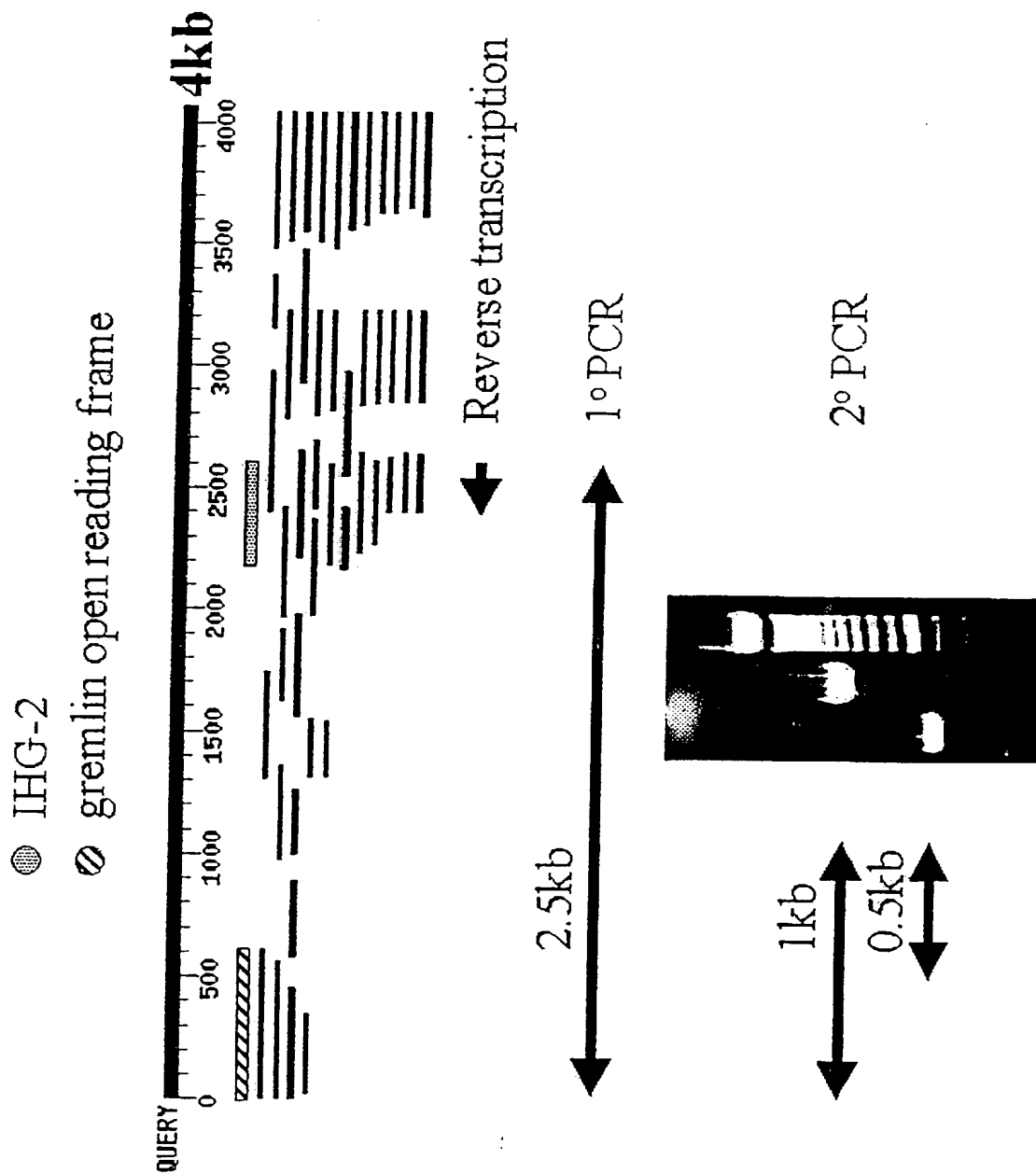


Fig. 13

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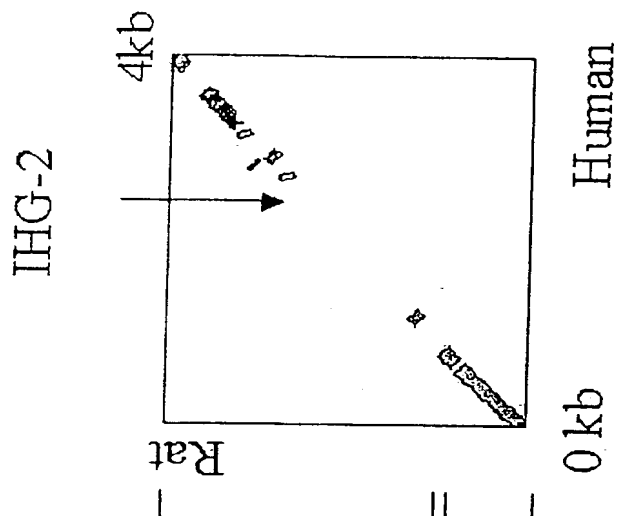


Fig. 14

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1 GCGGCCGCACTCAGCGCCACGCGTCGAAAGCGCAGGCCCGGAGGCCCGCCGCACTGACAGTATGAGCCGCACAG  
M S R T A  
76 CCTACACGGTGGGAGCCCTGCTTCTCCTCTTGGGGACCCTGCTGCCGGCTGCTGAAGGGAAAAAGAAAGGGTCCC  
Y T V G A L L L L L L G T L L P A A E G K K K G S Q  
151 AAGGTGCCATCCCCCGCCAGACAAGGCCAGACAATGACTCAGAGCAGACTCAGTCCGCCAGCAGCCTGGCT  
G A I P P P D K A Q H N D S E Q T Q S P Q Q P G S  
226 CCAGGAACCGGGGGCGGGGCCAAGGGCGGGGCATGCCATGCCCGGGGAGGAGGTGCTGGAGTCCAGCCAAGAGG  
R N R G R G Q G R G T A M P G E E V L E S S Q E A  
301 CCCTGCATGTGACGGAGCGCAATACCTGAAGCGAGACTGGTGCAAAACCCAGCCGCTTAAGCAGACCATCCAGC  
L H V T E R K Y L K R D W C K T Q P L K Q T I H E  
376 AGGAAGGCTGCAACAGTCGCACCATCATCAACCGCTTCTGTTACGGCCAGTGCAACTCTTTCTACATCCCCAGGC  
E G C N S R T I I N R F C Y G Q C N S F Y I P R H  
451 ACATCCGGAAGGAGGAAGGTTCTTTTCTGCTCCTTCTGCAAGCCCAAGAAATCACTACCATGATGGTCA  
I R K E E G S F Q S C S F C K P K K F T T M M V T  
526 CACTCAACTGCCCTGAACACAGCCACCTACCAAGAAGAGAGTACACAGTGTGAAGCAGTGTCTGTCATAT  
L N C P E L Q P P T K K K R V T R V K Q C R C I S  
601 CCATCGATTTGGATTAAAGCCAATCCAGGTGCACCCAGCATGTCTTAGGAATGCAGCCCCAGGAAGTCCCAGACC  
I D L D  
676 TAAACAACCCAGATTCTTACTTGGCTTAAACCTAGAGGCCAGAAGAACCCCGAGTGCCTCCTGGCAGGAGCCTG  
751 CTGTGCGTAGTTCGTGTGCATGAGTGTGGATGGGTGCCTGTGGGTGTTTTAGACACCAGAGAAAACACAGTCT  
826 CTGCTAGAGAGCACTCCCTATTTTGTAAACATATCTGCTTAATGGGGATGTACCAGAAACCCACCTCACCCCGG  
901 CTCACATCTAAAGGGCGGGCGGTGGTCTGGTCTGACTTTGTGTTTTGTGCCCCCTCTGGGGACCAAGATCTC  
976 CTTTCGGAATGAATGTTTCATGGAAGAGGCTCCTCTGAGGGCAAGAGACCTGTTTAGTGCTGCATCTCGACATGGA  
1051 AAAGTCCTTTTAACTGTGCTTGCATCCTCCTTCTCCTCCTCCTCACAATCCATCTCTTTAAGTTGATAGT  
1126 GACTATGTCACTAATCTCTTGTGTTGCCAAGGTCTCTAAATTAATCACTTAACCATGATGCAAAATGTTTTCA  
1201 TTTTGTGAAGACCTCCAGACTCTGGGAGAGGCTGGTGTGGGCAAGGACAAGCAGGATAGTGGAGTGAGAAAGGG  
1276 AGGGTGGAGGGTGAGGCCAAATCAGGTCCAGCAAAAGTCAGTAGGGACATTGCAGAAGCTTGAAGGCCAATACC  
1351 AGAACACAGGCTGATGCTTCTGAGAAAGTCTTTCTTAGTATTTAACAGAACCCAGTGAACAGAGGAGAAATGA  
1426 GATTGCCAGAAAGTGAATTAACCTTTGGCCGTGCAATCTGCTCAAACTTAACACCAAACTGAAACATAAATCTG  
1501 ACCACTCCTATGTTTCGGACCCAAGCAAGTTAGCTAAACCAAACTCCTCTGCTTTGTCCCTCAGGTGGAATA  
1576 GAGAGGTAGTTTGAACCTCTGTCATAGGGGTGGGAATTAATCAAAACCCACAGAGGCTGAAATTCCTAATACCT  
1651 TTCCTTTATCGTGGTTATAGTCAGCTCATTTCCTATCCACTATTTCCCATATGCTTCTGAGAGCCACTAAGTCTG  
1726 ATTGATAAAGATCCTGCCTCTGCTGAGTGTACCTGACAGTAAGTCTAAAGATGARAGAGTTAGGGACTACTCTG  
1801 TTTTAGCAAGARATATTKTGGGGGTCTTTTGTGTTAACTATTGTCAGGAGATTGGGCTARAGAGAAGACGACGA  
1876 GAGTAAGGAATAAAGGGRATTGCCTCTGGCTAGAGAGTAAGTTAGGTGTTAATACCTGGTAGAAATGTAAGGGA  
1951 GACTCCTCCCTTTCTTTATGTCTCACTAGGATCTGAGGGGACCTGTTAGGAGAGCATAGCATCATGATGTA  
2026 TTAGCTGTTCATCTGCTACTGGTGGATGGACATAACTATTGTAACCTATTCACTATTACTGGTAGGCACTGTCC  
2101 TCTGATTAACTTGGCCTACTGGCAATGGCTACTTAGGATTGATCTAAGGGCCAAAGTGCAGGGTGGGTGAACCT  
2176 TATTGTAACCTTGGATTGGTTAACTGTTTCTCAAGCCTGAGGTTTATATACAACTCCCTGAATACTCTTT  
2251 TTGCTTGTATCTTCTCAGCTCCTAGCCAAGTCTATGTAATATGGAACCAAACTGCAGACTTGAGATTCA  
2326 GTTCCGATCAAGGCTCTGGCATTGAGAGAACCTTGCAACTCGAGAAGCTGTTTTATTCGTTTTGTTTTGA  
2401 TCCAGTGTCTCTCCATCTAACAACCTAAACAGGAGCCATTTCAAGCGGGAGATATTTTAAACACCCAAATGTG  
2476 GGTCTGATTTTCAACTTTTAACTCACTACTGATGATCTCAGCTAGGCGAATTTGTCCAAACACATAGTGTG  
2551 TGTGTTTTGTATACACTGTATGACCCACCCCAATCTTGTATTGTCCACATTCTCCAAACATAAGCACAGAG  
2626 TGGATTAAATTAAGCACACAAATGCTAAGCGCAATTTTGAGGGTGGGAGAGAAGAAAGGGAAGAGCTGAAA  
2701 ATGTAACCAACACAGGGAGGAAAAATGACATTGAGAACCAGCAAACTGAATTTCTCTTGTGTTTTAACTC  
2776 TGCCACAAGAATGCAATTTCTGTTAATGGAGATGACTTAAGTTGGCAGCAGTAATCTCTTTTAGGAGCTTGATCC  
2851 ACAGTCTTGCACATAAGTGCAGATTGGCTCAAGTAAAGAGAATTTCTCAACACTAATCTCACTGGGATAATCA  
2926 GCAGCGTAACCTCCATAAAGCATATCACTAGCCAAAGAGGGAAATATCTGTTCTTCTACTGTGCTTATATAA  
3001 GACTAGTACAAATGTGGTGTGCTTCCAACCTTCAATGAAAATGCCATATCTATACCATATTTATTCTGAGTCAC  
3076 TGATGATGTAATGATATATTTTTTCAATATTATAGTAGAATATTTTATGGCAAGATTTTGTGGTCTTGATCAT  
3151 ACCATTAAAAATAATGCCAAACACCAATATGAATTTATGATGTACACTTTGTGCTGGCATTAAAGAAAAAA  
3226 ACACACACTCTGGAAGTCTGTAAGTTGTTTTTGTACTGTAGGCTTCAAAGTTAAGAGTGAAGTGAAGAAATC  
3301 TGGAGGAGAGGATAATTTCCACTGTGTGGAATGTGAATAGTTAAATGAAAGTTATGTTTATTTAATGTAATAT  
3376 TACTTCAAATCCTTTGGTCACTGTGATTCAAGCATGTTTTCTTTTCTCCTTTATATGACTTCTCTGAGTTGG  
3451 GCAAGAAGAGCTGACACACCGTATGTTGTAGAGTCTTTTATCTGGTCAGGGGAAACAAATCTTGACCCAGC  
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3676 TGATGACTAGTTCACACATAAAGTCTTTTAAAGGAGAAATCTAAATGAAAGTGGATAAACAGAACATTTATA  
3751 AGTGATCAGTTAATGCCTAAGAGTGAAGTAGTTCTATTGACATTCCTCAAGATATTTAATATCACTGCATTAT  
3826 GTATTATGTCTGTTAAATCATTTAAACCGGCAAGAAATATATAGACTATGAGGTACCTTGCTGTGTAGGAGG  
3901 ATGAAAGGGGAGTTGATAGTCTCATAAACTAATTTGGCTTCAAGTTTCAATCTGTAAGTGAATTTAATTT  
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Fig. 15

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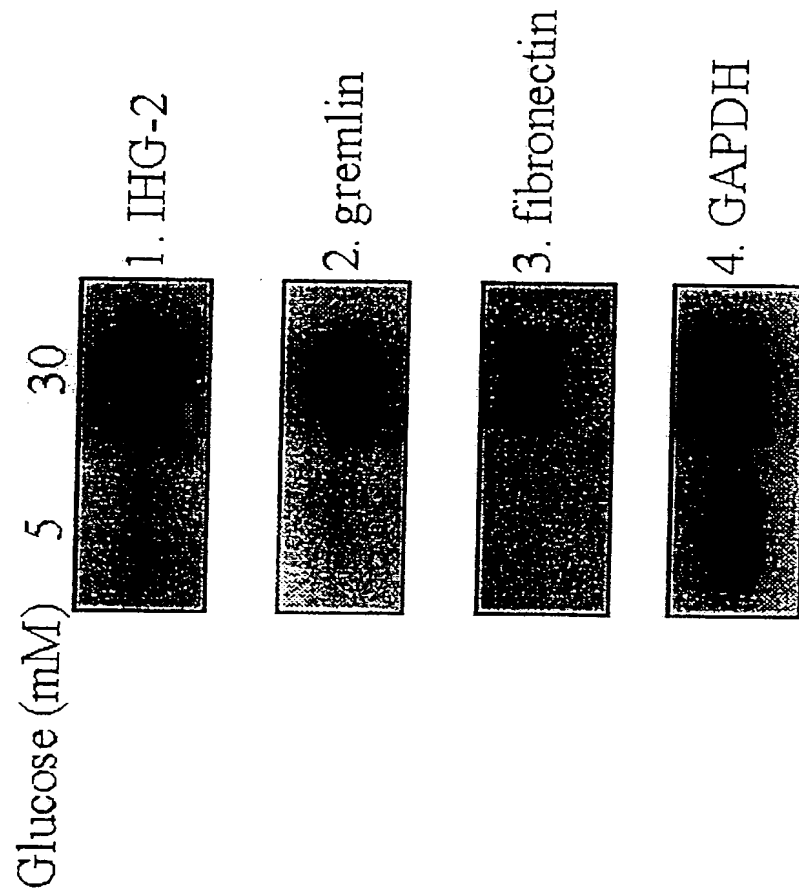


FIG. 16

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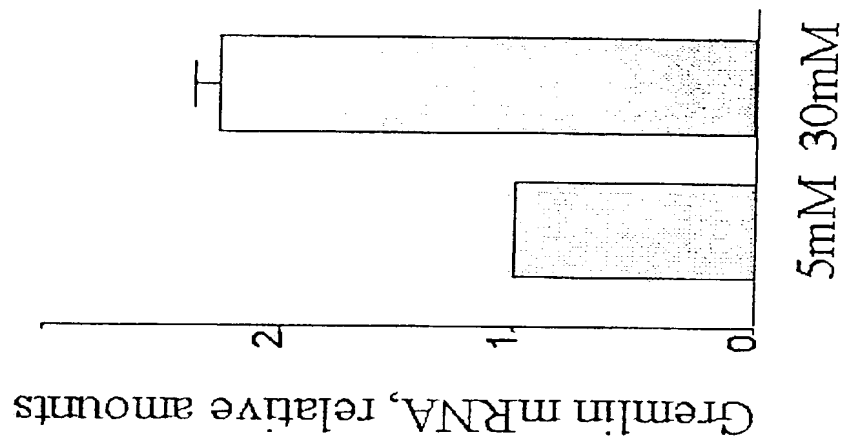


FIG. 17

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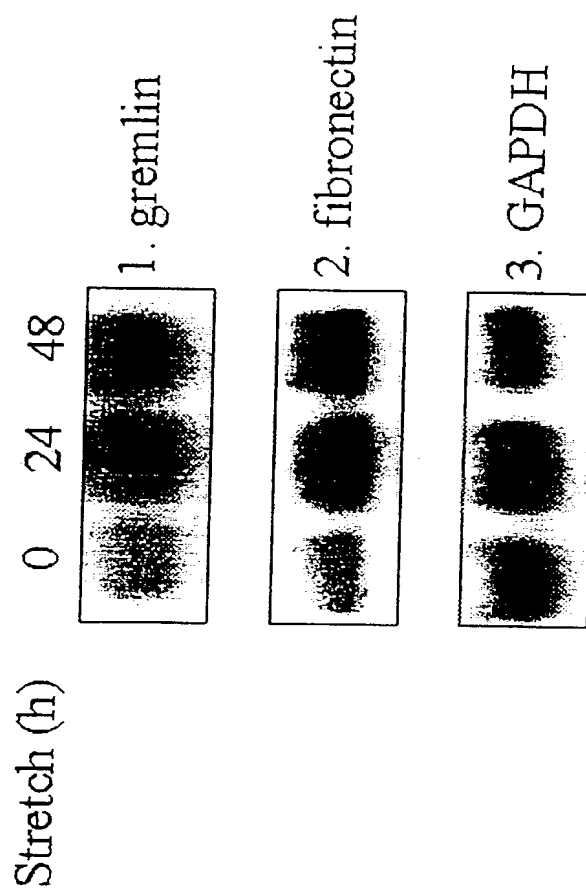


FIG. 18



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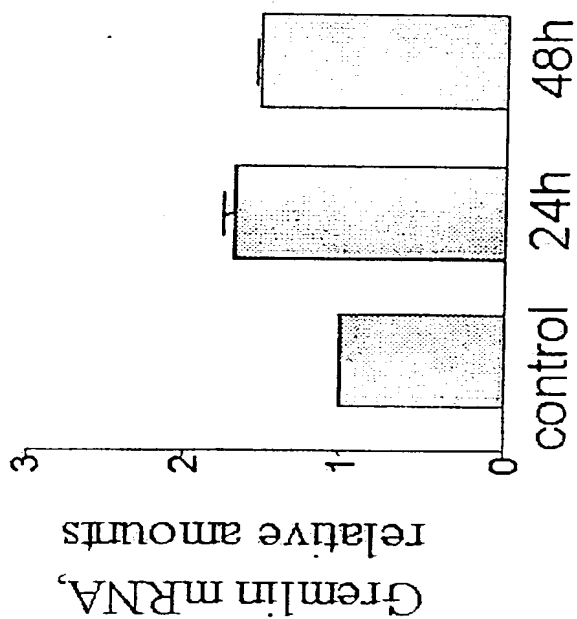


FIG. 19

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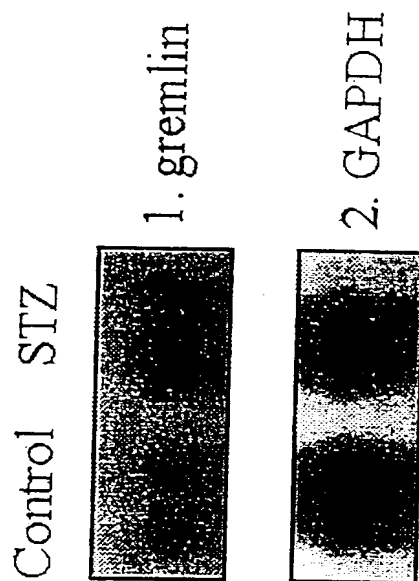


FIG. 20

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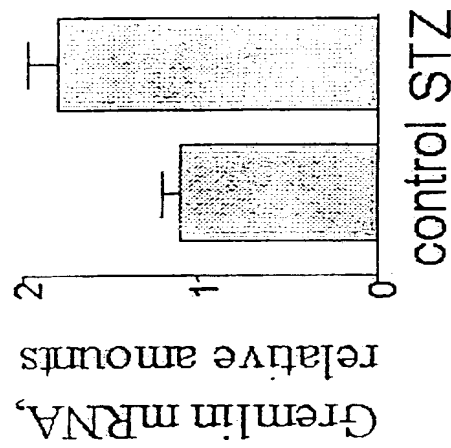


FIG. 21

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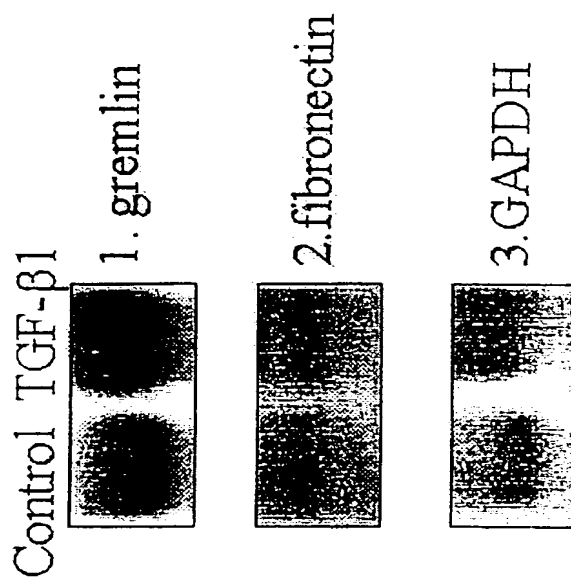


Fig. 22

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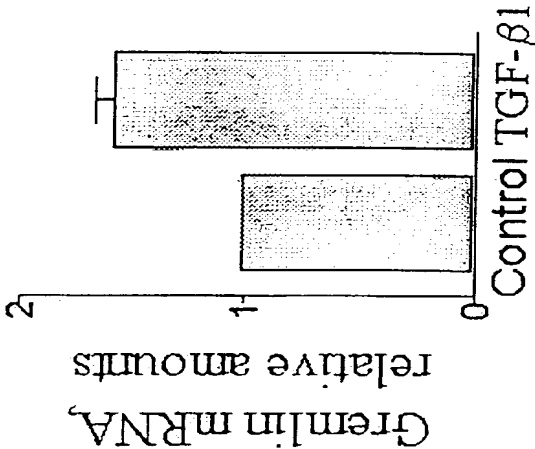


Fig. 23

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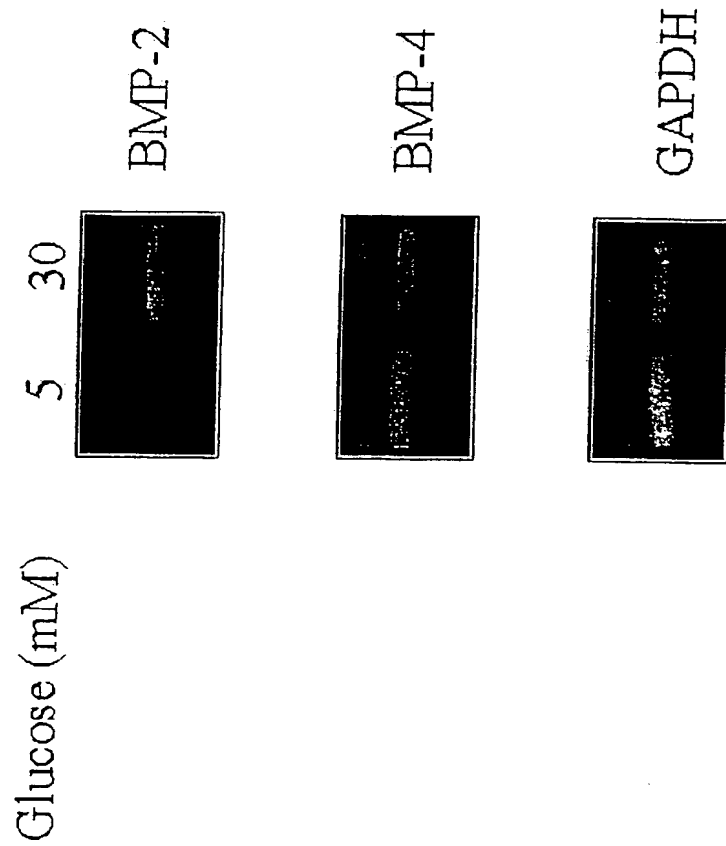


Fig. 24

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1377-0170P

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## COMBINED DECLARATION AND POWER OF ATTORNEY FOR PATENT AND DESIGN APPLICATIONS

As a below named inventor, I hereby declare that: my residence, post office address and citizenship are as stated next to my name; that I verily believe that I am the original, first and sole inventor (if only one inventor is named below) or an original, first and joint inventor (if plural inventors are named below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

Insert Title: → Identification of genes having a role in the presentation of diabetic nephropathy

the specification of which is attached hereto. If not attached hereto,

Fill in Appropriate  
Information —  
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Specification  
Attached:

the specification was filed on \_\_\_\_\_ as  
United States Application Number \_\_\_\_\_ ;  
and amended on \_\_\_\_\_ (if applicable); and/or  
the specification was filed on February 28, 2000 as PCT  
International Application Number PCT/IE 00/00026 ; and was  
amended under PCT Article 19 on \_\_\_\_\_ (if applicable)

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

I do not know and do not believe the same was ever known or used in the United States of America before my or our invention thereof, or patented or described in any printed publication in any country before my or our invention thereof or more than one year prior to this application, that the same was not in public use or on sale in the United States of America more than one year prior to this application, that the invention has not been patented or made the subject of an inventor's certificate issued before the date of this application in any country foreign to the United States of America on an application filed by me or my legal representatives or assigns more than twelve months (six months for designs) prior to this application, and that no application for patent or inventor's certificate on this invention has been filed in any country foreign to the United States of America prior to this application by me or my legal representatives or assigns, except as follows.

I hereby claim foreign priority benefits under Title 35, United States Code, §119 (a)-(d) of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed:

Insert Priority  
Information:  
(if appropriate)

Prior Foreign Application(s)			Priority Claimed	
→ <u>990157</u> (Number)	<u>Ireland</u> (Country)	<u>February 26, 1999</u> (Month / Day / Year Filed)	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No
_____ (Number)	_____ (Country)	_____ (Month / Day / Year Filed)	<input type="checkbox"/> Yes	<input type="checkbox"/> No
_____ (Number)	_____ (Country)	_____ (Month / Day / Year Filed)	<input type="checkbox"/> Yes	<input type="checkbox"/> No
_____ (Number)	_____ (Country)	_____ (Month / Day / Year Filed)	<input type="checkbox"/> Yes	<input type="checkbox"/> No

I hereby claim the benefit under Title 35, United States Code, §119(e) of any United States provisional application(s) listed below.

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(if any)

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_____ (Application Number)	_____ (Filing Date)

All Foreign Applications, if any, for any Patent or Inventor's Certificate Filed More than 12 Months (6 Months for Designs) Prior to the Filing Date of This Application:

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→ _____	_____	_____
_____	_____	_____

I hereby claim the benefit under Title 35, United States Code, §120 of any United States and/or PCT application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States and/or PCT application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose information which is material to patentability as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application:

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Application(s):  
(if any)

→ _____ (Application Number)	_____ (Filing Date)	_____ (Status — patented, pending, abandoned)
_____ (Application Number)	_____ (Filing Date)	_____ (Status — patented, pending, abandoned)

I hereby appoint the following attorneys to prosecute this application and/or an international application based on this application and to transact all business in the Patent and Trademark Office connected therewith and in connection with the resulting patent based on instructions received from the entity who first sent the application papers to the attorneys identified below, unless the inventor(s) or assignee provides said attorneys with a written notice to the contrary:

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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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Sole Inventor:  
Insert Name of  
Inventor →  
Insert Date this  
Document is Signed

Insert Residence  
Insert Citizenship →

Insert Post Office  
Address →

Full Name of Second  
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see above

Full Name of Third  
Inventor, if any  
see above

Full Name of Fourth  
Inventor, if any  
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Full Name of Fifth  
Inventor, if any  
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\* DATE OF SIGNATURE